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(54) Title: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF

(57) Abstract

Mutants of the human PAI-1 protein are described which are inhibitors of neutrophil elastase or are inhibitors of vitronectin (Vn)-dependent cell migration. These mutants preferably comprise one or two amino acid substitutions in the reactive center loop of PAI-1, particularly at positions 331 and 346 of the mature protein. These mutants are notable in being resistant to inactivation by elastase, having high affinity for Vn, or both properties. These mutant proteins as pharmaceutical compositions are used to inhibit elastase in a subject, thereby treating a number of disorders associated with elastase activity, most notably emphysema, ARDS, inflammatory lung injury and cystic fibrosis. The mutants which interact with Vn are used to inhibit cell migration in a subject, thereby treating diseases or conditions associated with undesired cell migration and proliferation, particularly of smooth muscle cells. Such conditions include atherosclerosis, post angioplasty restenosis, fibrosis associated with chronic inflammation or chemotherapy, tumor invasion and metastasis and conditions in which angiogenesis is pathogenic. Also disclosed are peptides of such mutant proteins, mutant-specific antibodies, nucleic acid molecules, particularly DNA, encoding the mutant protein and host cells transformed by such nucleic acids.

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MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF

BACKGROUND OF THE INVENTION

Field of the Invention

The invention in the field of biochemistry and medicine relates to compositions comprising mutant proteins of plasminogen activator inhibitor-type 1 (PAI-1) which have the capacity to inhibit the enzyme elastase and to inhibit vitronectin (Vn)-dependent migration of cells. This invention also relates to uses of these proteins for the treatment of diseases and disorders associated with elastase activity or in which migration and migration-driven proliferation of cells have pathophysiologic consequences.

Description of the Background Art

1. PLASMINOGEN ACTIVATORS

Plasminogen activators (PAs) are specific serine proteinases that activate the proenzyme plasminogen, by cleavage of a single Arg-Val peptide bond, to the enzyme plasmin (Saksela O, *Biochim Biophys Acta* (1985) 823:35-65). Two plasminogen activators are found in mammals, tissue-type PA (tPA) and urokinase-type PA (uPA) (Saksela O *et al*, *Annu Rev Cell Biol* (1988) 4:93-126). These enzymes are thought to influence critically many biological processes, including vascular fibrinolysis (Bachmann E, *Thromb Haemost* (1987) 10:227-265), ovulation (Hsueh AJW *et al*, In: Haseltine FP *et al*, eds, *Meiotic Inhibition: Molecular Control of Meiosis* New York: Liss 1988:227-258), inflammation (Pollanen J *et al.*, *Adv Cancer Res* (1991) 57:273-328), tumor metastasis (Dano K *et al.*, *Adv Cancer Res* (1985) 44:139-266), angiogenesis (Moscatelli D *et al.*, *Biochim Biophys Acta* (1988) 948:67-85), and tissue remodeling (Saksela, *supra*). The regulation of PAs is a complex process controlled on many levels. The synthesis and release of PAs are governed by various hormones, growth factors, and cytokines (Saksela, *supra*; Dano *et al.*, *supra*). Following secretion, PA activity can be regulated both positively and negatively by a number of specific protein-protein interactions. Activity can be enhanced or concentrated by interactions with fibrin (Hoylaerts M *et al.*, *J Biol Chem* (1982) 257:2912-2919), the uPA receptor (uPAR) (Ellis V *et al.*, *Semin Thromb Hemost* (1991) 17:194-

200), the tPA receptor (tPAR) (Hajjar KA *et al.*, *J Biol Chem* (1990) 265:2908-2916), or the plasminogen receptor (Plow EF *et al.*, *Thromb Haemost* (1991) 66:32-36).

PA activity can be downregulated by specific PA inhibitors (PAIs) (Lawrence, D.A *et al.*, In: *Molecular Biology of Thrombosis and Hemostasis*, Roberts, H.R. *et al.*, (Eds.), Marcel Dekker Inc., New York, chapter 25, pp. 517-543 (1995)). In addition, PA activity is dependent on its location or microenvironment and may be different in solution (*e.g.*, circulating blood) as compared to a solid-phase (*e.g.*, on a cell surface or in the extracellular matrix (ECM)). The overall activity of the PA system is determined by the interactions among these various elements and the balance between the opposing activities of enzymes and inhibitors.

The PAIs have become recognized as critical regulators of the PA system. The identification of an efficient inhibitor of tPA in endothelial cells (ECs) was first reported in 1983 (Loskutoff DJ *et al.*, *Proc Natl Acad Sci USA* (1983) 80:2956-2960). Four kinetically relevant PAIs are currently recognized: PAI type 1 (PAI-1), initially described as the endothelial cell PAI; PAI type 2 (PAI-2), also referred to as placental PAI; PAI type 3 (PAI-3), also known as activated protein C (APC) inhibitor and proteinase nexin 1 (PN-1), also called glia-derived neurite-promoting factor. The present invention is directed in particular to PAI-1.

2. OTHER SERINE PROTEINASES

Elastase is a serine proteinase released by activated neutrophils and macrophages and monocytes. During inflammatory responses, neutrophils are activated and release elastase leading to tissue destruction through proteolysis. In the lung, elastase degrades elastic tissues and leads to emphysema. Elastase is also a compounding factor in cystic fibrosis (CF) and in both adult and infant acute respiratory distress syndrome (ARDS). Elastase has also been implicated in TNF-mediated inflammation (Massague, J. *et al.*, *Annu. Rev. Biochem.* *62*:515-541 (1993) and HIV infection (Bristow, C.L. *et al.*, *International Immunol.* 7:239-249 (1995)).

Elastase has a broader spectrum of reactivity than plasminogen activators each of which acts preferentially on a precursor substrate to activate it.

The natural defense to elastase is a protein called α1 anti-trypsin (α_1AT) or α1 proteinase inhibitor ((α_1PI). Patients who are deficient in α_1AT are prone to emphysema, especially smokers. Furthermore, smoking provokes inflammation. In such α1AT deficiencies, the enzyme is present (CRM$^+$) but is functionally impaired. In addition, even in individuals with normal enzyme, smoking directly inactivates α_1AT. Therefore, an improved inhibitor of elastase would be highly desirable for the prevention of emphysema in susceptible subjects or for reversal of the pathophysiological process leading to this an other related diseases.

3. SERPINS

The major PAIs belong to the serine proteinase inhibitor (serpin) gene superfamily which includes many proteinase inhibitors in blood as well as other proteins with unrelated or unknown function (Huber R *et al.*, *Biochemistry* (1989) 28:8951-8966). The serpins share a common tertiary structure and have evolved from a common ancestor. Serpins regulate many processes including coagulation, fibrinolysis, complement activation, ovulation, angiogenesis, inflammation, neoplasia, viral pathogenesis and allergic reactivity.

Current models of serpin structure are based on x-ray crystallographic studies of one member of the family, α_1AT (reviewed in Huber *et al.*, *supra*). An interesting feature of the structure of a modified form of α1AT, cleaved in its reactive center (Loebermann H *et al.*, J Mol Biol (1984) 177:531-557), is that the two amino acid residues that normally constitute the reactive center (Met-Ser bond), are found on opposite ends of the molecule, separated by almost 70Å. This is shown for PAI-1 in Figure 2 and can be compared to the active structure modeled in Figure 1. Relaxation of a strained configuration takes place upon cleavage of the reactive-center peptide bond, rather than a major rearrangement of the inhibitor structure. In this model, the reactive center is part of an exposed loop, also called the strained loop. Upon cleavage, this loop moves or "snaps back," becoming one of several central strands in a major β sheet structure. This

transformation is accompanied by a large increase in thermal stability, presumably as a result of the reconstitution of the six-stranded β sheet A.

Synthetic peptides homologous to the reactive-center loops of serpins, when added in *trans*, incorporate into their respective molecules, presumably as a central strand of the major β sheet structure and increase the thermal stability of the molecule like that observed after cleavage at the reactive center. This structural change converts the serpin from an inhibitor to a substrate for its target proteinase (Carrell RW *et al.*, Nature (1991) 353:576-578; Bjork I *et al.*, *J Biol Chem* (1992) 267:1976-1982).

Serpins act as suicide inhibitors, reacting only once with their target proteinase to form a sodium dodecyl sulfate (SDS)-stable complex. These complexes can dissociate to yield free active enzyme together with a cleaved inhibitor similar to that seen in the α1AT crystal structure (Carrell RW *et al.*, In: Barrett AJ, *et al.* eds., *Proteinase Inhibitors*. Amsterdam: Elsevier Science Publishers 1986:403-420) and modeled in Figures 1 and 2 for PAI-1.

Serpins interact with their target proteinase by providing a "bait" amino acid residue in the reactive center which is thought to mimic the normal substrate of the enzyme and to associate via its side-chain atoms with the specificity crevice, or S1 site, of the enzyme (Huber *et al.*, *supra*; Carrell *et al.*, *supra*; Shubeita HE *et al.*, *J Biol Chem* (1990) 265:18379-18385; York JD *et al.*, *J Biol Chem* (1991) 266:8495-8500; Sherman PM *et al.*, *J Biol Chem* (1992) 267:7588-7595). The bait amino acid is designated the P1 residue. The amino acids toward the N-terminal side of the scissile reactive-center bond are labeled in order P1, P2, P3, *etc.*, and the amino acids on the carboxyl side are labeled P1', P2', *etc.* (Carrell *et al.*, 1986, *supra*). The amino acid residues in the reactive center loop of PAI-1 (residues 332-351) are shown below labeled according to the foregoing naming convention. Also noted are the numerical positions in the full sequence of mature PAI-1:

332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351
P15	P14	P13	P12	P11	P10	P9	P8	P7	P6	P5	P4	P3	P2	P1	P1'	P2'	P3'	P4'	P5'
Gly	Thr	Val	Ala	Ser	Ser	Ser	Thr	Ala	Val	Ile	Val	Ser	Ala	Arg	Met	Ala	Pro	Glu	Glu

The complex between serpins and their target proteinases is thought to be covalently linked via an ester bond between the active-site serine residue of the proteinase and the new C-terminal end of the P1 residue, forming an acyl-enzyme complex (Lawrence DA *et al.*, *J Biol Chem* (1995) 279:25309-25312). The association between inhibitor and proteinase also involves regions other than the P1 residue of the serpin and other than the catalytic site of the proteinase, based on the characterization of two recombinant PA mutants in which six or seven amino acids were deleted from the catalytic domains. These mutant PAs were almost completely refractory to inhibition by PAI-1, suggesting that the residues distant from the active site are nevertheless critical for the interaction with PAI-1 (Madison EL *et al.*, *Nature* (1989) 339:721-724; Adams DS *et al.*, *J Biol Chem* (1991) 266:8476-8482).

4. PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1 (PAI-1)

PAI-1 (see Table 1) is considered one of the principal regulators of the PA system. It is a single chain glycoprotein with a molecular weight of 50kDa (Van Mourik JA *et al.*, *J Biol Chem* (1984) 259:14914-14921) and is the most efficient inhibitor known of the single- and two-chain forms of tPA and of uPA (Table 1) (Lawrence D *et al.*, Eur J Biochem (1989) 186:523-533). PAI-1 also inhibits plasmin and trypsin (Hekman CM *et al.*, Biochemistry (1988) 27:2911-2918) and also inhibits thrombin and activated protein C, though with much lower efficiency.

Table 1

SUMMARY OF CHARACTERISTICS OF PAI-1

Other Names	Sources	2nd Order Rate Constants ($M^{-1} s^{-1}$)		Other ligands
Endothelial PAI	*In vivo*	uPA	9.0×10^6	Vitronectin
Platelet PAI	platelets	tctPA	2.7×10^7	Heparin
Fast-acting PAI	smooth muscle	sctPA	4.5×10^6	Fibrin
β-Migrating PAI	LPS-activated	APC	1.1×10^4	
	endothelium	Plasmin	6.6×10^5	
	In vitro:	Trypsin	7.0×10^5	
	many cells types	Thrombin	10^3 -2×10^5	

Abbreviations: LPS, lipopolysaccharide: sctPA. single-chain tPA: tctPA. two-chain tPA: APC. activated protein C

PAI-1 is present in plasma at very low concentrations, ranging from 0 to 60ng/ml (average of about 20ng/ml or 0.5nM) (Declerck PJ *et al.*, *Blood* (1988) 71:220-225) and a reported half-life of about 6-7 minutes (Vaughan DE *et al.*, *Circ Res* (1990) 67:1281-1286). In a study comparing the clearance of two distinct forms of PAI-1 (active and latent; see below), the active form was cleared biphasically (half-lives of 6 and 25 minutes), whereas latent PAI-1 was cleared with a half-life of only 1.7 minutes (Mayer EJ *et al.*, Blood (1990) 76:1514-1520).

PAI-1 is present in platelets and other tissues and is produced by many cell types in culture (Erickson LA *et al.*, *J Clin Invest* (1984) 74:1465-1472; Sawdey MS *et al.*, *J Clin Invest* (1991) 88:1346-1353; Krishnamurti C *et al.*, *Semin Thromb Hemost* (1992) 18:67-80). *In vivo*, the primary extravascular source of PAI-1 appears to be vascular smooth muscle cells (SMCs) (Loskutoff DJ, *Fibrinolysis* (1991) 5:197-206). During endotoxemia or other pathological conditions, ECs become a major site of PAI-1 synthesis (Pyke C *et al.*, *Cancer Res* (1991) 51:4067-4071; Schneiderman J *et al.*, *Proc Natl Acad Sci USA* (1992) 89:6998-7002; Keeton M *et al.*, *Am J Pathol* (1993) 142:59-70).

Plasma PAI-1 is present as a complex with vitronectin (Vn) or S protein (Declerck PJ *et al.*, *J Biol Chem* (1988) 263:15454-15461). PAI-1 is also associated with Vn in the ECM in culture and may be involved in maintaining the

integrity of the cell substratum *in vivo* (Mimuro J *et al.*, *Blood* (1987) 70:721-728; Mimuro J *et al.*, *J Biol Chem* (1989) 264:5058-5063).

The major source of plasma PAI-1 is not known but is likely to be vascular SMCs, though a contribution from the platelet pool cannot be excluded. PAI-1 functions efficiently in solution and when bound to surfaces ("solid phase"), and it is likely that PAI-1 regulates fibrinolysis in both environments.

(a) PAI-1 Protein Structure and Function (See Figures 1-4)

PAI-1 cDNA encodes a protein of 402 amino acids that includes a typical secretion signal sequence (Ny *et al.*, *supra*; Ginsburg *et al.*, 1986, *supra*). Mature human PAI-1 isolated from cell culture is composed of two variants of 381 and 379 amino acids in approximately equal proportions. These two forms, likely arising from alternative cleavage of the secretion signal sequence, provide proteins with overlapping amino-terminal sequences of Ser-Ala-Val-His-His and Val-His-His-Pro-Pro (portion of SEQ ID NO:2 and 3) (Lawrence *et al.*, 1989, *supra*). This latter sequence is generally referred to as mature PAI-1.

PAI-1 is a glycoprotein with three potential N-linked glycosylation sites containing between 15 and 20% carbohydrate (Van Mourik JA *et al.*, *supra*). Mature PAI-1 contains no cysteine residues, facilitating efficient expression and isolation of recombinant PAI-1 from *E. coli*. PAI-1 produced in *E. coli*, although nonglycosylated, is functionally very similar to native PAI-1. Recombinant PAI-1 can be isolated from *E. coli* in an inherently active form (see below), which contrasts with PAI-1 purified from mammalian cell culture (Lawrence *et al.*, 1989, *supra*; Hekman *et al.*, 1988, *supra*).

(b) Active and Latent Conformation

PAI-1 exists in an active form as it is produced by cells and secreted into the culture medium and an inactive or latent form that accumulates in the culture medium over time (Hekman CM *et al*, *J Biol Chem* (1985) 260:11581-11587; Levin EG *et al*, Blood (1987) 70:1090-1098). The active form spontaneously converts to the latent form with a half-life of about 1 h at 37°C (Lawrence *et al.*, *supra*; Hekman *et al.*, *supra*; Levin EG *et al*, 1987, *supra*).

The latent form can be converted into the active form by treatment with denaturants, negatively charged phospholipids or Vn (Lambers *et al*, *supra*,

Hekman *et al*, *supra*; Wun T-C *et al*, *J Biol Chem* (1989) 264:7862-7868). Latent PAI-1 infused into rabbits became reactivated *in vivo* by an unknown mechanism. The reversible interconversion between the active and latent structures, presumably due to a conformational change, is a unique feature of PAI-1 as compared to other serpins. The latent form appears to be more energetically favored.

The three-dimensional structure of the latent form of PAI-1 has been solved.. In this structure the entire N-terminal side of the reactive center loop is inserted as the central strand into β sheet A (Fig. 2) (Mottonen *et al.*, *supra*) which explains the increased stability (Lawrence, D.A. *et al.*, *Biochemistry* *33*:3643-3648 (1994)) as well as the lack of inhibitory activity. The structure of active PAI-1 is still unknown. It has been proposed that the reactive center in active PAI-1 is exposed as a surface loop, in contrast to its position in the latent structure (Fig. 1).

(c) The Reactive-Center Loop (RCL)

The RCL region of PAI-1 has been the subject of extensive mutational analysis which demonstrated the importance of the P1 bait residue in inhibitor function, whereas the surrounding amino acids play a less critical role. Random mutagenesis of the P3, P2, and P1 residues and the P1 and P1' residues, respectively, clearly demonstrated that either arginine or lysine at P1 is essential for PAI-1 to function as an effective inhibitor of uPA (York *et al.*, 1991, *supra*; Sherman *et al.*, 1992, *supra*). Residues surrounding P1 can modulate PAI-1 inhibitor activity by up to two orders of magnitude and can alter target proteinase specificity. The P1' site is surprisingly tolerant of amino acid substitutions with the exception of proline which caused almost total loss of function. When an 18 amino acid segment of PAI-1 encompassing most of the RCL was replaced with the same region from PAI-2, antithrombin III, or a serpin consensus sequence, most of the requirements for PAI-1 specificity (apart from the P1 residue), were found to lie outside the RCL sequence. All three chimeras remained efficient inhibitors of tPA and uPA, and the antithrombin III chimera was not a significantly improved inhibitor of thrombin. Furthermore, the specific sequence of the RCL, the region inserted into β sheet A in the latent PAI-1 structure (Fig.1, see above), was not critical for the conversion between the active and latent conformations of PAI-1. Hence, loop insertion depends more on the flexibility of β sheet A than on the

specific amino acid residues in the loop. Finally, binding to Vn was not affected by these substitutions in the RCL. The P4' and P5' residues on the C-terminal side of the reactive-center bond have also been replaced with only a small effect on PAI-1 activity.

(d) Interactions with Vitronectin (Vn)

The adhesive glycoprotein Vn is a 72 kDa glycoprotein present in plasma at micromolar concentrations and associated with many tissues. Like PAI-1, Vn can exist in multiple conformational states. Vn is involved in a wide variety of physiological responses, including cell adhesion, complement activation, thrombosis, and plasma clearance of proteinase-inhibitor complexes (Tomasini, B.R. *et al.* (1991) *Prog. Hemost. Thromb. 10*, 269-305).

PAI-1 in plasma or in the subcellular matrix is stabilized by Vn. Vn-bound PAI-1 in solution is approximately twice as stable as unbound PAI-1. On ECM the half-life of PAI-1 can be >24 h (Mimuro *et al.*, *supra*). Most of the PAI-1 found in platelets appears to be latent, although this point is controversial (Lang IM *et al.*, Blood (1992) 80:2269-2274). Platelets contain Vn (Preissner KT *et al.*, Blood (1989) 74:1989-1996), which could act to reactivate latent platelet PAI-1 (Wun *et al.*, *supra*). Platelet PAI-1 may be a major factor in the resistance of platelet-rich thrombi to thrombolysis (Fay WP *et al.*, *Blood* (1994) 84:351-356). Consistent with this, anti-PAI-1 antibodies enhance clot lysis when contacted with platelet-rich thrombi *in vitro* (Levi M *et al.*, Circulation (1992) 85:305-312; Braaten JV *et al.*, Blood (1993) 81:12901299).

Vn is thought to localize PAI-1 to the ECM where it regulates local proteolytic activity (Mimuro *et al.*, 1987, *supra*). Views concerning the interaction of PAI-1 with Vn are controversial probably due to the conformational variability of both proteins. The controversy is directed to both the nature and affinity of binding of these two molecules (Sigurdardottir O *et al.*, *Biochim Biophys Acta* (1990) 1035:56-61; Kost C *et al.*, *J Biol Chem* (1992) 267:12098-12105; Seiffert D *et al.*, *Biochim Biophys Acta* (1991) 1078:23-30; Salonen E-M *et al.*, *J Biol Chem* (1989) 264:6339-6343). Controversy also surrounds the Vn binding site for PAI-1, which has been localized to the somatomedin B domain at the N-terminus (Seiffert D *et al.*, *J Biol Chem* (1991) 266:2824-2830) and to the C terminus of Vn

between residues 348 and 370 (Kost *et al.*, *supra*). Some of these conflicts may be explained by differences in affinity of binding of the active vs. latent form of PAI-1 with Vn and/or by differences in the relative abundance of PAI-1 conformers in various PAI-1 preparations.

Recent studies of the serpin mechanism of inhibition indicate that it follows a multi-step process that requires an exposed RCL (Shore, J.D. *et al.*, (1994) *J. Biol. Chem. 270*, 5395-5398; Lawrence, D.A. *et al.*, (1995) *J Biol. Chem. 270*, 25309-25312; Fa, M. *et al.*, (1995) *Biochem. 34*:13833-13840; Wilczynska, M. *et al.*, (1995) *J. Biol. Chem. 270*:29652-29655). Upon association with a target proteinase the serpin RCL is cleaved at its P_1-$P_{1'}$ bond and this is followed by a rapid insertion of the RCL into β-sheet A yielding the stable serpin-proteinase complex. As shown by the present inventors (see Examples) a PAI-1 Vn binding epitope on the edge of β-sheet A is sensitive to this conformational change in β-sheet A, as well as to similar changes associated with conversion of PAI-1 to the latent form or cleavage in the RCL by a non-target proteinase. This sensitivity may provide a way to ensure the expression of PAI-1 activity at specific sites of action. For example, Vn is thought to localize PAI-1 to the ECM where it regulates local proteolytic activity (Mimuro *et al.*, *supra*). In this situation it may be beneficial to permit only functionally active PAI-1 to bind to Vn. On a cell surface an inactive ligand it can be internalized and degrades. However, this type of regulation may not be as efficient on the less dynamic ECM. Therefore, to prevent Vn from becoming saturated with inactive forms of inhibitor, a system may have evolved that is sensitive to the conformational state of PAI-1, which is closely linked to its activity state.

In addition to stabilizing active PAI-1, Vn alters PAI-1 specificity, converting it to an efficient inhibitor of thrombin (Ehrlich *et al*, *supra*; Keijer, J. *et al.*, *Blood* (1991) 78:1254-1261). Vn-bound PAI-1 has a 270-fold greater rate constant toward thrombin than does free PAI-1, dependent upon the source of the Vn. Although all forms of Vn can bind PAI-1, only Vn isolated under physiological conditions is able to stimulate PAI-1 to inhibit thrombin (Naski, M.C. *et al.*, *J Biol Chem* (1993) 268:12367-12372). Vn also enhances the clearance of PAI-1-thrombin complexes by the low density lipoprotein receptor-related protein

(LRP) (Stefansson, S. *et al.*, (1996) *J Biol. Chem. 271*:8215). PAI-1 does not appear to contribute significantly to thrombin inhibition in plasma *in vivo*, although local concentrations of PAI-1 may have significant effects. Vn also stimulates the inhibition of tPA by PAI-1, but to a much less dramatic extent (Keijer *et al.*, *supra*; Edelberg JM *et al.*, *J Biol Chem* (1991) 266:7488-7493). Vn can partially restore the reduced inhibitory activity of PAI-1 RCL mutants toward tPA.

(e) Interactions with Thrombin

Given that PAI-1 is expressed at sites of inflammation and released from platelet granules upon activation, it may under these conditions be a relevant inhibitor of thrombin. While PAI-1 alone is a rather poor inhibitor of thrombin, PAI-1-Vn complexes have greatly augmented ability to inhibit thrombin (Naski. *et al.*, *supra*). Vn is present in connective tissue extracellular matrices and released from platelets upon their activation. Thrombin-PAI-1 complexes form on endothelial cell ECM, which can be inhibited with antibodies to Vn (Ehrlich, H.J. *et al.*, (1991) *J. Cell Biol. 115*, 1773-1781). While these authors speculated that the thrombin:PAI-1 interaction might promote PA activity by neutralizing PAI-1, this interaction may also mediate cellular clearance of thrombin. Such clearance would resemble that of tPA and uPA whose endocytosis and degradation via several members of the LDL receptor family are promoted after complex formation with PAI-1 (Nykjaer, A. *et al.*, (1992) *J. Biol. Chem. 267*, 14543-14546 (Orth, K. *et al.*, (1992) *Proc. Natl. Acad. Sci. USA 89*, 7422-7426; Stefansson, S. *et al.*, (1995), *J. Cell Sci. 108*: 2361-2369).

(f) Clinical Significance of PAI-1 and its Interactions

Increased levels of circulating PAI-1 are associated with thrombotic disease, including myocardial infarction and deep vein thrombosis (Juhan-Vague I *et al.*, *Thromb Res* (1984) 33:523-530; Hamsten A *et al.*, N Engl J Med (1985) 313:1557-1563; Wiman B *et al.*, J Lab Clin Med (1985) 105:265-270; Paramo JA *et al.*, BMJ (1985) 291:573-574; Nilsson IM *et al.*, BMJ (1985) 290:1453-1456; Aznar J *et al.*, Br Heart J (1988) 59:535-541; Angles-Cano E *et al.*, J Lab Clin Med (1993) 121:646-653). Reduced postoperative fibrinolytic activity has been correlated with increased PAI-1 activity immediately following surgery (Kluft C *et al.*, Scand J Clin Lab Invest (1985) 45:605-610), apparently mediated by a plasma

factor that stimulates PAI-1 production and secretion from vascular ECs (Kassis J *et al.*, Blood (1992) 80:1758-1764). Consistent with these observations, the overproduction of PAI-1 in transgenic mice results in venous thrombosis primarily in the extremities (Erickson LA *et al.*, Nature (1990) 346:74-76). In contrast, a prospective study found no correlation between PAI-1 levels and vascular disease (Ridker PM *et al.*, Circulation (1992) 85:1822-1827).

Three cases of partial or complete PAI-1 deficiency have been reported in humans and were associated with abnormal bleeding. In one case, normal PAI-1 antigen was detected, but PAI-1 activity was significantly reduced (Schleef RR *et al.*, *J Clin Invest* (1989) 83:1747-1752), whereas in another, both PAI-1 antigen and activity levels in plasma were markedly reduced with normal levels in platelets (Dieval J *et al.*, Blood (1991) 77:528-532). A complete deficiency of platelet and plasma PAI-1 in a 9-year-old Amish girl was associated with a moderate bleeding disorder. The patient was homozygous for a 2 base pair insertion at the end of exon 4 of the PAI-1 gene (Fay WP *et al.*, N Engl J Med (1992) 327:1729-1733) which results in a frameshift leading to a truncated PAI-1 protein and an unstable mRNA. The deficiency is inherited as an autosomal recessive disorder. Although heterozygous parents and siblings all had plasma PAI-1 activity and antigen in the normal range, they were consistently lower than homozygous normal family members. The lack of developmental and other abnormalities in this patient was considered surprising. The correlation of complete PAI-1 deficiency with abnormal bleeding clearly demonstrates that importance of PAI-1 in the regulation of hemostasis. Given the young age of the above patient, however, an additional important *in vivo* role of PAI-1 in the control of ovulation or tumor metastasis cannot yet be excluded (Pollanen *et al.*, *supra*; Liu Y-X *et al.*, Eur J Biochem (1991) 195:549-555).

(g) <u>Clearance Receptors</u>

The LDL receptor-related protein (LRP) is a cell surface receptor (family with four members) which acts as a general clearance receptor for a diverse set of ligands, including proteinase inhibitor complexes. For review, see Strickland, D.K. *et al.*, *FASEB J.* *9*:890-898 (1995)) Binding to LRP results in the uptake of PAI-1-proteinase complexes into cells and destruction in the lysosomal

compartment. While LRP is found on all cells, these receptors are present at higher levels in liver and on the epithelial lining of the lungs.

(h) Cell Migration

Cell migration is a tightly controlled process which depends on the coordination of many factors. Migrating cells and cells with invasive phenotypes express high levels of uPA. Processes such as angiogenesis and metastasis can be blocked by proteinase inhibitors. Inactivation of the gene for uPA in mice prevents arterial stenosis due to neointima formation following vascular trauma (Carmeliet, P. *et al.*, *Circulation 90*:1-144 (1994)). During wound healing vascular cells exhibit an increase in the expression of the Vn receptor (VnR) integrin $\alpha_V\beta_3$ (Liaw L *et.al.*, *Circ Res* 77:665-72 (1995)). VnR permits cell motility on matrix proteins deposited at the wound. Specifically, migration into the wound area is facilitated by Vn which is deposited at the site by activated platelets or derived from plasma. Migrating vascular cells also show elevated expression of uPA and its receptor uPAR which co-localize with the VnR at focal contacts. As previously understood in the art, the PAs were thought to activate a generalized proteolytic cascade resulting in matrix destruction necessary for cellular migration and invasion. However, results obtained by the present inventors and presented herein suggest a more subtle role for PAs in regulating the expression of cryptic cell attachment sites.

SUMMARY OF THE INVENTION

The present invention provides mutants and variants of wild-type human PAI-1 (wtPAI-1) that have improved properties in the inhibition of serine proteinases, in particular elastase. These mutant PAI-1 molecules are more resistant to destruction by the proteinases to which they bind and therefore have improved therapeutic properties.

The nucleotide sequence (SEQ ID NO:1; the complementary strand is SEQ ID NO:10)) and amino acid sequence (including the signal sequence) (SEQ ID NO:2) of human PAI-1 is shown in Figure 3 and 4A. The full mature protein sequence (SEQ ID NO:3) is shown in Figures 4B.

The present invention is further directed to the use of PAI-1 and mutants and variants thereof for the inhibition of elastase activity. PAI-1 and its mutants are used to treat any of a number of diseases associated with elastase activity, including emphysema, CF and ARDS. Mutants of this invention are also used to inhibit Vn-dependent cell attachment, migration and subsequent proliferation, which processes are associated with diseases ranging from atherosclerosis and restenosis to tumor growth and metastasis and neovascularization.

Thus, the present invention is directed to a mutant protein of PAI-1 protein, which wild-type sequence of which is SEQ ID NO:3, which mutant inhibits neutrophil elastase or other elastase-like proteinases. Preferably the inhibition is such that no more than about one mole of the mutant protein are required to inhibit 1 mole of the elastase. More preferably no more than about two moles, four moles, ten moles, or most preferably 100 moles, of the mutant protein are required to inhibit 1 mole of the elastase.

Also provided is the above mutant protein having at least one amino acid substitution in the sequence from amino acid position 343 to 350 of SEQ ID NO:3, more preferably in positions 331-350. Preferred substitutions are at position 343, position 346 or both. A preferred substitutions at position 346 is Ala, Val, Asp, Phe or Gly. A preferred substitution at position 343 is Ala, Asp, Gly, Leu or Ile. In a preferred embodiment the mutant protein has both a substitution position 343 and 343 as above. Another preferred mutant protein differs from SEQ ID NO:3 by a single substitution of Val at position 346, a single substitution of Ala at position 343, or both. Also provided is a mutant protein having a substitution at 343, 346 or both, wherein the amino acid substituting at position 343: (a) renders the mutant protein resistant to cleavage by elastase after position 343, and (b) has side chains which do not interfere with the binding of the mutant protein to the elastase to form a mutant PAI-1:elastase complex.

A mutant protein as above may further include between one and four of the following additional amino acid substitutions in SEQ ID NO:3 which stabilize the protein: (a) His at position 150; (b) Thr at position 154; (c) L u at position 319; and (d) Ile at position 354. A preferred mutant includes all four of the above additional substitutions. Additional stabilizing substitutions include Leu at position

91 and Ile at position 372. Also preferred are mutants having additionally Arg at position 333 and/or 335 or at both 333 and 335. An additional substitution in this region is Gly at 331. PAI-1 mutants including any combination of the foregoing substitutions may be used as a stabilized form of the protein, in particular for use *in vivo*.

In another embodiment, the present invention is directed to a mutant protein of PAI-1 protein (SEQ ID NO:3) which is particularly useful for inhibiting the binding of PAI-1 to Vn. Such as mutant is characterized as being resistant to inactivation by the following proteinases: elastase, a plasminogen activator, plasmin, thrombin, cathepsin G, chymase, gelatinase A and B, stromelysin and a collagenase. Such an inhibitory PAI-1 mutant protein preferably has high affinity for Vn such that the binding of the mutant protein to a proteinase does not decrease the affinity of binding of the mutant protein to Vn more than about 100-fold relative to the affinity of wtPAI-1 to Vn.

The above mutant protein preferably has at least one amino acid substitution in the fragment from amino acid position 343 to position 350 of SEQ ID NO:3, more preferably from 331 to 350. One or more of the abovementioned substitutions at positions 343 and 346 (as well as at 331, 333 and 335) are preferably included in this embodiment. The mutant protein may have between one and four, preferably all four, of the following additional amino acid substitutions in SEQ ID NO:3: (i) His at position 150; (ii) Thr at position 154; (iii) Leu at position 319; and (iv) Ile at position 354.

In another embodiment is provided any mutant protein of PAI-1 protein (SEQ ID NO:3) which has a higher affinity for Vn than does wtPAI-1.

Shorter peptides which include at least the PAI-1 reactive center loop with the amino acid substitutions described above are also intended to be within the scope of this invention. Such peptides may be used a elastase inhibitors or cell migration inhibitors *in vitro* or *in vivo*. As elastase inhibitors, such peptides (or full length mutant proteins) are useful in methods of measuring or titrating elastase activity.

The present invention is also directed to a pharmaceutical composition useful for inhibiting elastase activity in a subject, comprising (a) a mutant protein

(or peptide) as described above, and (b) a pharmaceutically acceptable carrier or excipient.

Also provided is a pharmaceutical composition useful for inhibiting Vn-dependent cell attachment, migration and/or migration-induced cell proliferation in a subject, comprising (a) a mutant PAI-1 protein as described above and (b) a pharmaceutically acceptable carrier or excipient.

This invention is further directed to a method for inhibiting elastase in a subject having a disease or condition associated with pathogenic elastase activity, comprising administering to the subject an effective amount of a pharmaceutical composition as above. The disease or condition is preferably one selected from the group consisting of emphysema, acute respiratory distress syndrome, acute inflammatory lung injury, congenital alpha-1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, pancreatitis, periodontal disease, arthritis and HIV infection.

Also provided is a method for inhibiting cell attachment, migration and/or migration-induced cell proliferation in a subject having a disease or condition associated with undesired Vn-dependent cell attachment, migration and/or migration-induced proliferation, comprising administering to the subject an effective amount of (a) a pharmaceutical composition comprising wtPAI-1 protein and a pharmaceutically acceptable carrier or excipient; or (b) a pharmaceutical composition comprising a mutant PAI-1 protein as described above.

In the foregoing method, the inhibition is preferably directed to smooth muscle cells. In the foregoing method, the disease or condition is preferably atherosclerosis, post-balloon angioplasty vascular restenosis, neointima formation following vascular trauma, vascular graft restenosis, fibrosis associated with a chronic inflammatory condition, lung fibrosis, chemotherapy-induced fibrosis, wound healing with scarring and fibrosis, primary tumor growth, invasion or growth of a tumor metastasis, psoriasis, deep venous thrombosis, or a disease or condition in which angiogenesis is pathogenic.

This invention is further directed to a nucleic acid molecule, preferably, DNA encoding a mutant PAI-1 protein or peptide as described above. The nucleic acid molecule is preferably a variant of SEQ ID NO:1 or of a coding portion thereof. Also provided is a host cell transformed or transfected with a DNA

molecule as above which encodes a mutant PAI-1 protein or peptide. The invention includes methods for producing the mutant PAI-1 protein comprising culturing the transformed or transfected host cells under conditions wherein the mutant PAI-1 protein or peptide is expressed.

Also provided is an antibody, polyclonal or monoclonal, specific for an epitope of a mutant PAI-1 protein as described above, which epitope is not present on wtPAI-1 protein.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1-2 are models (ribbon diagrams)of active PAI-1 (Fig. 1) and RCL-cleaved (inactive) PAI-1 (Fig. 2). The PAI-1 main chain is shown in gray. Certain of the amino acid residues of the RCL are highlighted. Space filling models of the amino acid side chains of P1 (Arg 346), P1' (Met 347) and P9 (Ser 338) are shown in darker shades of gray. The approximate position of P16 (Ser 331)is indicated by a small black diamond.

Figure 3 shows the nucleotide sequence (SEQ ID NO:1) encoding human PAI-1 plus 5' and 3' untranslated regions from a particular clone. Also shown is the amino acid sequence of full length human PAI-1 including the signal peptide.

Figures 4A-4B show the amino acid sequence of the PAI-1 protein. SEQ ID NO:2 (Fig. 4A) includes the signal peptide whereas SEQ ID NO:3 (Fig. 4B) is the mature protein. Preferred residues for substitution to generate mutants are indicated in Fig. 4A as is the reactive center loop (RCL) region.

Figure 5 is a graph showing the inhibition of neutrophil or pancreatic elastase by wtPAI-1, α1AT or P1 Ala-PAI-1. The ordinate represents the residual enzymatic activity following 30 min. incubation with increasing concentrations of the inhibitor.

Figure 6 shows the results of polyacrylamide gel electrophoresis (12.5% SDS-gels) of mixtures of elastase with wtPAI-1 or P1 Ala PAI-1. Lanes 1-3: neutrophil elastase. Lanes 1 & 4: elastase alone. Lanes 2 & 5: elastase + wtPAI-1. Lanes 3 & 6: elastase + P1 Ala PAI-1. The gels were stained with Coomassie blue . Bands can be seen representing the elastase enzyme, the inhibitor or the enzyme-inhibitor complex.

Figure 7 is a graph showing the effect of the PAI-1 P1 Ala mutant on internalization of ^{125}I-human neutrophil elastase by type II pneumocytes.

Figures 8 and 9 are a set of graphs showing endocytosis (Fig. 8) and degradation (Fig. 9) by pre-type II pneumocytes of active and active site-inhibited thrombin and effects of PAI-1 antibodies. ^{125}I-thrombin:PPACK (^{125}I-Th:PPACK) and active ^{125}I-thrombin (^{125}I-Th) each at 20 nM. Also shown in each panel are the effects of rabbit anti-mouse PAI-1 IgG (0.6 mg/ml) or normal rabbit IgG (Control IgG, 0.6 mg/ml) on active ^{125}I-thrombin. The results represent 3 experiments each performed in duplicate. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figures 10 and 11 are a set of graphs comparing the level of endocytosis (Fig. 10) and degradation (Fig. 11) of ^{125}I-thrombin in complex with serpins. Pre-type II pneumocyte cells were incubated with ^{125}I-thrombin in complex with the synthetic inhibitor Phe-Pro-Arg-chloromethyl ketone (^{125}I-Th:PPACK), HCII (^{125}I-Th:HCII), ATIII (^{125}I-Th:ATIII), α_1PI (^{125}I-Th:α_1PI) each at 16nM. The results represent 4 experiments. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figures 12 and 13 are a set of graphs comparing the level of endocytosis (Fig. 12) and degradation (Fig. 13) of ^{125}I-thrombin:PAI-1 complex inhibited by antagonists of LRP function. ^{125}I-thrombin:PAI-1 complex (10 nM) was incubated with cultured pre-type II pneumocyte cells in the presence of RAP (1μM), affinity purified LRP-1 antibodies (anti-LRP-1, 150μg/ml), affinity purified LRP-2 antibodies (anti-LRP-2, 150 μg/ml), a mixture of the LRP-1 and 2 antibodies (anti-(LRP-1+2)), 300 μg/ml) or antibody to a peptide corresponding to the cytoplasmic tail of LRP (anti-LRP-1 CD, 150 μg/ml). Specific endocytosis and degradation was determined by co-incubation with 500-fold molar excess of unlabeled thrombin:PAI-1. The results are representative of 2 experiments. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figures 14 and 15 are a set of graphs showing the binding of ^{125}I-thrombin:PAI-1 complex to LRP-1 (Fig. 14) and LRP-2 (Fig. 15). The binding was measured in the presence of increasing concentrations of unlabeled

thrombin:PAI-1, thrombin or PAI-1. The curves represent the best-fit of the data to a single class of sites. The results represent 4 experiments each performed in duplicate. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figures 16-19 are a set of graphs showing the effect of wild-type PAI-1, or a mutant of PAI-1 that is unable to bind Vn, on the endocytosis and degradation of ^{125}I-thrombin (Figures 16 and 18) or ^{125}I-uPA (Figures 17 and 19). Pre-type II pneumocyte cells were incubated with either wild-type PAI-1 ("wtPAI-1", 10nM) or mutant PAI-1 ("mPAI-1", 10nM) that is unable to bind Vn. ^{125}I-thrombin or ^{125}I-uPA (10 nM) incubated with cells in the presence or absence of RAP (1μM). Figures 16 and 17 show endocytosis while Figures 18 and 19 show degradation. The results represent 4 experiments each performed in duplicate. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figures 20 and 21 are a set of graphs showing endocytosis and degradation of ^{125}I-thrombin that has been pre-complexed to either wild-type PAI-1 (Fig. 20) or mutant PAI-1 (Fig. 21). Pre-type II pneumocyte cells were incubated with ^{125}I-Th:wtPAI-1 or ^{125}I-Th:mPAI-1 (1nnM complex). See Figure 16-19 for designation of groups. Where indicated, RAP (1μM) was added along with the complex. Endocytosis and degradation of each type of ^{125}I- complexes are shown. The results represent 2 experiments. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figures 22-25 are a set of graphs showing the effect of native or conformationally-altered Vn on the endocytosis and degradation of ^{125}I-thrombin (Figures 22 and 24) or ^{125}I-uPA (Figures 23 and 25) in the presence of wtPAI-1. Pre-type II pneumocytes were incubated with either native Vn ("nVn", 50 nM) or conformationally altered Vn (denatured="dVn", 50 nM). After washing the cells were incubated with wild-type PAI-1 (10nM) followed by addition of either ^{125}I-thrombin (10nM) or ^{125}I-uPA (10 nM). Figures 22 and 23 show endocytosis while Figures 24 and 25 show degradation. The results represent 3 experiments. Each plotted value represents the average of duplicate determinations with the range indicated by bars.

Figure 26 is a graph showing binding of recombinant active or latent wtPAI-1 to microtiter plates coated with purified native (nVn) or urea-denatured(dVn) Vn. Bound PAI-1 was detected with affinity purified, biotinylated, rabbit anti-PAI-1 antibodies and streptavidin conjugated to alkaline phosphatase Data points represent the average of at least four separate determinations for each sample ± S.E.M.

Figure 27 is a graph showing the binding of four additional forms of PAI-1 to nVn coated microtiter plates. These forms include PAI-1 in a stable complex with either uPA or tPA, cleaved PAI-1 that is uncomplexed but has a reconstituted β-sheet A, and PAI-1 annealed to a synthetic RCL peptide, which has an intact RCL that is not inserted into β-sheet A, but has a reconstituted sheet A due to insertion of the synthetic peptide to form strand 4 of sheet A (Kvassman, J., *et al.*, (1995) *J Biol. Chem.* 270, 27942-27947). The assay was performed as in Figures 26 with the same number of determinations.

Figure 28 is a graph showing binding of active wtPAI-1, covalent complexes of wtPAI-1-trypsin , or non-covalent PAI-1-anhydrotrypsin complexes to nVn coated microtiter plates. The assay was performed as in Figure 26, except that for analysis of the PAI-1-anhydrotrypsin complex binding to Vn, 1μM (final concentration) of anhydrotrypsin was included in all wells during the PAI-1 incubation step. Data points are as in Figure 26.

Figure 29 is a graph showing binding of recombinant active or latent wtPAI-1 and active or latent mutant PAI-1 Q123K to nVn coated microtiter plates. Assay and data points are as in Figure 26.

Figure 30 is a graph showing the binding of radiolabeled VnR to Vn and its competition by wtPAI-1 and PAI-1 mutants. The results represents three experiments performed in duplicate.

Figures 31 and 32 are a set of graphs showing the inhibition by PAI-1 and the P1 Ala mutant of the binding of VnR to Vn (Fig. 31) or fibronectin (Fig. 32) and its reversal by uPA. The results represent 2 experiments, each performed in duplicate.

Figures 33 and 34 are a set of graphs showing the inhibition by PAI-1 and mutants thereof of smooth muscle cell adhesion to Vn (Fig. 33) and fibronectin

(Fig. 34) and its reversal by uPA. The results represents 4 experiments performed in duplicate..

Figure 35 shows a functional assay for the binding of recombinant active wtPAI-1 to native or urea-purified Vn. The amount of active PAI-1 bound was determined functionally. Active wtPAI-1 binding to nVn (○); or uVn (●). Data points represent the average of at least four separate determinations for each sample ± the S.E.M, and the plots were generated with the GraFit program (Erithacus Software).

Figure 36 shows competitive inhibition of PAI-1 binding to immobilized nVn by solution-phase Vn. The amount of PAI-1 bound to nVn is plotted vs. the concentrations of solution-phase native or urea-purified Vn. PAI-1 bound was determined by ELISA. Competition of PAI-1 binding by nVn (○); or by uVn (●). Data points and generation of plots (four parameter logistic fit) were as described for Figure 35.

Figure 37 shows binding of recombinant active or latent wtPAI-1 to native Vn (nVn) or urea-purified Vn (uVn)-coated microplates. The amount of PAI-1 bound was determined by ELISA. Open symbols show PAI-1 binding to nVn and filled symbols indicate PAI-1 binding to uVn. Active PAI-1 (○, ●); Latent PAI-1 (□, ■). Data points and generation of plots were as for Figure 35.

Figure 38 shows the binding of active PAI-1 (○), PAI-1:tPA complex (Δ), PAI-1:uPA complex (□), PAI-1 in complex with the synthetic RCL peptide (∇), or PAI-1 cleaved by elastase (◇) to nVn. Assays were performed as in JBC Figure 3. Data points and generation of plots were as described for Figure 37.

Figure 39 shows binding of active wtPAI-1 (○), wtPAI-1-trypsin covalent complexes (Δ), or non-covalent PAI-1-anhydrotrypsin complexes (□) to nVn coated microplates. The assay was performed as in Figure 38, except that for analysis of the PAI-1-anhydrotrypsin complex binding to Vn, 1 μM (final concentration) of anhydrotrypsin was included in all wells during the PAI-1 incubation step. Data points represent the average of at least four separate determinations for each sample ± the S.E.M, and the plots for active PAI-1 ± anhydrotrypsin were generated as for Figure 37.

Figure 40 shows PAI-1 inhibition of ^{125}I-VNR binding to Vn. Plot of ^{125}I-VNR bound to Vn vs. the concentration of PAI-1 added. wtPAI-1 ( ), R346A-PAI-1 (•), and Q123K-PAI-1 (○). The data represent the average of 5 experiments performed in duplicate.

Figure 41 shows inhibition of ^{125}I-VNR binding to Vn by PAI-1 with or without uPA. ^{125}I-VNR bound to Vn in the presence of each competitor. The data represent the average of 2 experiments both performed in duplicate.

Figure 42A and 42B show attachment and migration of rabbit SMC on Vn. Fig. 42A shows the amount of cell attachment to Vn coated plates in the presence of each competitor. Fig. 42B shows the extent of cell migration through Vn coated Transwells in the presence of each competitor. The data represent the average of 5 experiments (Fig. 42A) or 3 experiments (Fig. 42B) all performed in duplicate.

Figure 43 shows migration of rabbit SMC through Matrigel coated Transwells with or without Vn. The extent of cell migration through Matrigel coated Transwells ± Vn in the presence of each competitor. The data represent the average of 3 experiments each performed in duplicate.

Figure 44 shows the effect of increasing concentrations of immobilized Vn (Vn) on SMC migration. Vn in TBS was coated onto Transwells at the indicated concentrations and incubated for 2 hours at 37°C after which the wells were blocked using 3% BSA in TBS. SMC in serum free DMEM media were added to the top Transwell chamber and allowed to migrate for 8 hours. After which the cell migration was assessed (See Example VI).

Figure 45 shows the effect of increasing concentrations of PAI-1 on SMC migration on Vn. Vn was coated onto Transwells as in Figure 44. SMC in serum free DMEM media were added to the top Transwell chamber and allowed to attach for 30 min before PAI-1 was added to the cell layer. SMC were allowed to migrate for 8 hours after which the migration was assessed as noted above.

Figure 46 shows that Vn in serum enhances SMC migration on Matrigel. Transwells were coated with Matrigel (1:20 dilution in TBS) for 2 hours at 37°C after which the Transwells were washed and incubated with TBS, bovine serum or purified native Vn (0.2 mg/ml in TBS). Cells were allowed to attach for 30 min

before PAI-1 (1 µM) was added (fourth bar). Migration was assayed as noted above.

Figure 47 shows the effect of an RGD peptide on the attachment of SMC to native Vn. Native Vn (1 µg/ml in TBS) was coated onto 96 well plates in incubated for 2 hours at 37°C, after which plates were blocked with 3% BSA in TBS. SMC were added to wells in the absence or presence of the peptides GRGDSP (100 µM in DMEM) or GRGESP 100 µM in DMEM), or LM609 (0.5 µg/ml in TBS) or wtPAI-1 (1 µM in DMEM). Cells were allowed to attach for 45 min before assay was terminated.

Figure 48 shows the effect of PAI-1 and RGD peptides on attachment of SMC and bovine aortic epithelial (BAE) cells to native Vn. Native Vn was coated as above. SMC and BAE were allowed to attach to the wells in the presence of the peptide GRGDSP (100 µM in DMEM) or PAI-1 (1 µM in DMEM)for 45 min before prior to termination of the assay.

Figures 49A and 49B shows the effect of RGD peptides (Fig. 49A) and PAI-1 (Fig. 49B) on attachment of SMC and BAE to native Vn. Native Vn was coated as above at 1 µg/ml. SMC and BAE were allowed to attach to the wells in the presence of increasing concentrations of GRGDSP or PAI-1 for 45 min before the assay was terminated.

Figures 50A-50C show the effect of PAI-1, its mutants on cytokine-induced angiogenesis. Angiogenesis in the chicken chorioallantoic membrane (CAM) was stimulated using basic fibroblast growth factor (Brooks, P. C. *et al.*, 1994, *Science*, *264*:569-571). Figure 50A is a quantitative representation of angiogenesis in response to 2µM active PAI-1 (the stabilized 14-1B mutant) and 2µM latent PAI-1 (the wild type sequence). Figure 50B shows dose dependent inhibition of angiogenesis by active PAI-1 (the 14-1B mutant) at 1, 0.1 and 0.01 µM. Figure 50C compares the angiogenesis inhibiting activity 2µM "wt" PAI-1 (the 14-1B 1 mutant, wherein "wild-type" refers to its activity, not its sequence) with two PAI-1 mutants each having one additional amino acid substitution: R346A which binds Vn but is unable to inhibit uPA and Q123K which inhibits uPA but does not bind Vn.

Figure 51 shows a comparison of the cellular degradation of human neutrophil elastase (NEL) in complex with either PAI-1 or α1-proteinase inhibitor (α_1PI). The cellular clearance of a PAI-1 mutant able to inhibit neutrophil elastase) complexed to NEL (NEL:PAI-1) was compared to a complex of NEL with α_1PI (NEL-α_1PI). Preformed complexes of ^{125}I-NEL (25 nM) with PAI-1 or α1-PI were added to mouse embryo fibroblasts (MEF) cultures. Degradation of the complexes were assessed as described (Stefansson, S. *et al.*, 1996, *J. Biol. Chem.* *271*:8515-8220). The degradation of NEL-PAI-1 is inhibited by adding the receptor associated protein (RAP, 1 μM)), which antagonizes the binding of all ligands to the LDL-related protein (LRP). NEL degradation was also inhibited by the lysosomal degradation inhibitor, chloroquine (150 μM).

Figure 52 compares the inhibition of human NEL enzymatic activity by PAI-1 mutants and α_1-proteinase inhibitor. NEL (2nM) was incubated with increasing concentrations of "α_1PI" (●), a PAI-1 mutant having two amino acid substitutions from the wild type - "V343A R346V" (○), the 14-1B mutant of PAI-1 additionally having two substitutions - "V343A, R346V 14-1B" (■) and the 14-1B mutant of PAI-1 additionally having one substitution - "R346A 14.1B" (□). Residual activity of the elastase was measured by monitoring hydrolysis of N-methoxysuccinyl-Ala-Ala-Pro-Val p-nitroanilide at 405nm.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

One of the present inventors and colleagues previously used site directed mutagenesis and other methods to produce and characterize a large number of mutations in the PAI-1 reactive center loop (RCL) (Sherman *et al.*, 1992, *supra*; Sherman *et al.*, 1995, *supra*). The present inventors have now made or identified new mutants in the RCL of PAI-1 which confer on PAI-1 new and useful properties, in particular (a) the ability to interact with and inhibit elastase, an activity which is lacking in native PAI-1 and (b) the ability to inhibit Vn-associated cell migration. These properties are the basis for the new uses for these mutants described below, for which purposes wild type PAI-1 ("wtPAI-1") or other proteinase inhibitors are less well suited or not useful at all.

The present invention therefore provides novel compositions in the form of mutants of PAI-1 with increased stability as proteinase inhibitors, in particular, as inhibitors of elastase. Secondary to their inhibition of elastase, these mutants promote the uptake and clearance of elastase (or the elastase-PAI-1 complexes) by LDL-related protein clearance receptors. Hence, use of these compositions enhances the removal of elastase from sites of potential or actual injury. The disclosed mutants effectively neutralize elastase at sites of inflammation or injury.

Because of the role of elastase in emphysema, cystic fibrosis (CF) and in acute respiratory distress syndrome (ARDS) in both adult and infant as well as in other conditions discussed below, the present invention provides methods for treating these or any other diseases associated with pathogenic activation of elastase, which method comprises administering either PAI-1 or the PAI-1 mutants described herein.

Two functional classes of mutant PAI-1 molecules are contemplated within the scope of the present invention: mutants which inhibit neutrophil elastase (or other elastases) and mutants which inhibit Vn-dependent cell migration. Preferred mutants possess both these characteristics.

Mutants which Inhibit Elastase

A preferred elastase-inhibiting PAI-1 mutant has the following characteristics:

(1) PAI-1 molecule of full length or having between 1 and 14 or its N-terminal amino acid truncated;

(2) has an amino acid substitution at the P1 site, the P4 site or both, as further delineated below;

(3) inhibits neutrophil elastase with a second order rate constant of at least $10^5 M^{-1} sec^{-1}$ with a stoichiometry of at least 2:1 at physiological salt concentrations and pH in the colorimetric assay described below.

Elastase inhibitory activity is defined as follows: no more than about 100 moles of the inhibitor are required to inhibit 1 mole of the elastase. Preferably no more than about 4 moles, more preferably, no more than about 2 moles and most preferably about 1 mole of the mutant protein is/are required to inhibit 1 mole of elastase.

A preferred substitution at P1 is Ala (R346A) or Val (R346V), although another substitutions, *e.g.*, Met (α_1AT has Met at this position) or Asp, is acceptable. The amino acid substitutions described herein are designated interchangeably as, for example, "P1 Ala", which indicates the position in the PAI-1 reactive center as being the P1 site, or R346A which indicates Arg is replaced by Ala at position 346 of PAI-1, SEQ ID NO:3, using the single letter amino acid code.

As shown in the Examples, below, pancreatic elastase is not inhibited by wtPAI-1, pancreatic elastase but is inhibited by the P1 Ala PAI-1 mutant. According to the results shown in Figure 6, a complex is formed between P1 Ala PAI-1 and elastase but not between wtPAI-1 and elastase. All of the wtPAI-1 is cleaved and thus inactivated by interacting with elastase, which explains its lack of inhibitory action.

Such inactivation of PAI-1 by elastase was also shown by Lawrence, D.A. *et al.*, *J. Biol. Chem.* 269:27657-27662, (1994). In fact, others have published that PAI-1 is not an inhibitor of elastase (Levin EG *et al.*, *J Cell Biol* (1987) 105:2543-2549). Shubeita *et al.* (*supra*) actually tried to modify PAI-1 to become an inhibitor of elastase and failed.

A mutant which included a replacement of P1 Arg by Ala, in combination with the wild type Met at P1' was described earlier by the present inventors and their colleagues (Sherman *et al.*, 1992, *supra*). In Figure 4 of that reference, it was shown that such a mutant lost the ability to inhibit uPA. This same mutant was later found to lack inhibitory activity toward tPA and thrombin (Sherman *et al.*, 1995, *supra*, at Figures 1 and 2). It is important to note that these described mutants were different from the mutants of the present invention in that the PAI-1 protein contained seven additional amino acids added to its N-terminus Met-Thr-Met-Ile-Thr-Asn-Ser (SEQ ID NO:4) (Sherman *et al.*, 1992, *supra*, at page 7590, column 2, last paragraph). Furthermore, Shubeita H.E. *et al. J. Biol. Chem.* 1990, *265*:18379-85, tried to change the P1 site in PAI-1 to inhibit elastase by using the α_1AT amino acid sequence into PAI-1 but found no inhibition.

The reason that the P1 Ala mutant inhibits elastase but not tPA or uPA is thought to be a function of the interaction with the specificity site (S1) of the

proteinase (though the inventors do not wish to be bound by any particular mechanistic interpretation). This S1 site of the proteinase is the primary determinant of substrate specificity. Depending on the size and hydrophobicity of the S1 site, it prefers to accommodate one type of amino acid or another. tPA and other PAs prefer basic residues at P1 (Arg or Lys). Elastase prefers small hydrophobic resides like Ala and Val. Hence, by a judicious choice of amino acids in the reactive center of the PAI-1 mutant, it is possible to select a substitution or combination of substitutions that optimize interaction with the elastase S1 site while preventing inactivation of the inhibitor and thereby maximizing it inhibitory capacity and ability to promote clearance of the elastase.

The substitution at the P4 site must be one which results in a protein which is not cleaved after the P4 residue by elastase. For this, it is useful to substitute for the Val at this position in the wtPAI-1. This resistance to inactivation permits the mutant to successfully inhibit elastase. Thus, a preferred amino acid substituent (a) is resistant to cleavage by elastase at this site, *i.e.*, does not act as a substrate site for elastase and (b) at the same time does not present side chains which interfere with the interaction and binding of PAI-1 to elastase to form a complex such that elastase activity is inhibited and the complex is efficiently cleared. Stated otherwise, the substituting amino acid at P4 should present a poor fit as a primary (substrate) site for elastase without distorting other subsite contacts which are needed for interaction and successful inhibition.

Preferred amino acids at P4 are small, such as Ala and Gly, though somewhat larger residues such as Leu and Ile are also contemplated. The amino acid may be charged, such as Asp which should make that site less amenable to cleavage by elastase.

If the P4 site is substituted, for example, with Ala, a larger number of possible substitutions at P1 are expected to result in a molecule with the desired inhibitory properties. The efficiency or rate of inhibition (second order rate constant) is expected to will be highest with Val at P1.

<u>Mutations which Inhibit Cell Migration</u>

A preferred PAI-1 mutant for inhibition of cell migration is any one which has high affinity for Vn and thereby allows the blockade of integrin (Vn receptor)

attachment to Vn. wtPAI-1 has this property. A second characteristic of such a mutant is that it is resistant to inactivation by a proteinase, most preferably, elastase, plasminogen activators, plasmin, thrombin, cathepsin G, chymase, gelatinase A and B, stromelysin and collagenase Any mutants which fulfill these criteria are intended.

A mutant protein or peptide with "high affinity" for Vn is defined as one in which binding to the proteinase target does not cause a significant loss of affinity for Vn (due to conformation change of the PAI-1 protein or peptide). Loss of affinity for Vn is defined as an increase in Kd of more than about 100 times the Kd of the wtPAI-1. For example, where the Kd of wtPAI-1 for Vn is about 10nM in a conventional assay, a preferred mutant will have Kd for Vn of about 100nM or lower after binding the protease, more preferably a Kd of 10nM or lower.

The property of resistance to inactivation cleavage by a proteinase upon binding to and inhibiting the proteinase is best achieved by a PAI-1 mutation in the RCL, preferably at the P1 site. A preferred mutant is P1 Ala. Alternatively, or additionally, a substitution at P4 which inhibits proteinase cleavage after the P4 site is also preferred, for example P4 Ala.

As stated above, a fragment of PAI-1 which has the requisite elastase-inhibiting or migration-inhibiting activity is within the scope of this invention. Such a fragment generally has most of the amino acids of full length PAI-1, and preferably does not have more than the 14 N-terminal amino acids cleaved. However, if it is later discovered that other fragments of PAI-1 maintain the requisite biochemical functions, then mutants of those fragments in accordance with the description above are within the scope of this invention.

Also included is a mutant of a longer polypeptide which has the delineated properties of PAI-1 along with the particular characteristics of the mutants described herein. Thus, for example, the N-terminal 30 amino acids of PAI-1 have been replaced with the N-terminal 50 amino acids of α1AT, resulting in a polypeptide that is longer by 20 amino acids than PAI-1 but retains biochemical properties of PAI-1. Substitution mutants of such a longer molecule of the type described above are also intended, provided that such mutants inhibit elastase or inhibit cell migration.

In addition to the aforementioned amino acid substitutions which bestow on PAI-1 the desirable characteristics for utility in accordance with the present invention, additional amino acid substitutions are known which stabilize PAI-1 (Berkenpas, M. *et al.*, *EMBO J.* *14*:2969-2977, 1995)). Preferred compositions will optionally include, in addition to substitutions at P1 and P4 sites, four additional substitutions at positions 150, 154, 319 and 354 of SEQ ID NO:3 as in the mutant designated 14-1B by Berkenpas *et al.*, *supra*. These substitutions are N150H, K154T, Q319L, M354I.

The list below summarizes (non-exclusively) preferred PAI-1 mutants. The amino acid residues shown are at positions P4-P4' in the RCL (corresponding to residues 343 to 350 of SEQ ID NO:3).

		343 344 345 346 347 348 349 350
wtPAI-1		Val-Ser-Ala-Arg-Met-Ala-Pro-Glu
Mutants		
1.	P1Ala (R346A)	Val-Ser-Ala-Ala-Met-Ala-Pro-Glu
2.	P1Val (R346V)	Val-Ser-Ala-Val-Met-Ala-Pro-Glu
3.	P1Gly (R346G)	Val-Ser-Ala-Gly-Met-Ala-Pro-Glu
4.	P1Asp (R346D)	Val-Ser-Ala-Asp-Met-Ala-Pro-Glu
5.	P4Ala(V343A)	Ala-Ser-Ala-Arg-Met-Ala-Pro-Glu
6.	P4Asp (V343D)	Asp-Ser-Ala-Arg-Met-Ala-Pro-Glu
7.	P4Gly (V343G)	Gly-Ser-Ala-Arg-Met-Ala-Pro-Glu
8.	P4Leu (V343L)	Leu-Ser-Ala-Arg-Met-Ala-Pro-Glu
9.	P4Ile (V343I)	Ile-Ser-Ala-Arg-Met-Ala-Pro-Glu
10.	P4AlaP1Val (V343A, R346V)	Ala-Ser-Ala-Val-Met-Ala-Pro-Glu
11.	P4AlaP1Ala (V343A, R346A)	Ala-Ser-Ala-Ala-Met-Ala-Pro-Glu
12.	P4AlaP1Asp (V343A, R346D)	Ala-Ser-Ala-Asp-Met-Ala-Pro-Glu
13.	R346A plus N150H,K154T,Q319L,M354I	
14.	R346V plus N150H,K154T,Q319L,M354I	
15.	V343A,R346V plus N150H, K154T, Q319L, M354I	
16.	V343A,R346D plus N150H, K154T, Q319L, M354I	

Also intended are mutants such as these listed below additionally having one or more of the following two substitutions: T333R (Arg at residue 333 in place of Thr), and A335R (Arg at 335 in place of Ala) and, optionally, S331G (Gly at residue 331 in place of Ser). The importance of these positions, in particular the 333 position, is described in Lawrence, D.A. *et al.*, *J. Biol. Chem.* 269:27657-27662 (1994), which is incorporated by reference in its entirety.

While the present disclosure is directed primarily to human PAI-1, it is to be understood that homologues of PAI-1 from other species, and mutants thereof, that possess the characteristics disclosed above are intended within the scope of this invention. In particular, the PAI-1 protein (or DNA) from other mammalian species may be used for the same purposes as human PAI-1 in the treatment of diseases or conditions in humans or in other mammalian species.

As noted above, the present invention also includes peptides which include at least that portion of the sequence which contains the substitution or substitutions, and which possess the requisite biochemical and biological activity such as elastase inhibition. Such peptides may be produced using well-known synthetic methods for the synthesis of polypeptides of desired sequence on solid phase supports and their subsequent separation from the support. Methods for solid phase peptide synthesis are well-described in the following references, hereby incorporated by reference: Merrifield, B., *J. Amer. Chem. Soc. 85*:2149-2154 (1963); Merrifield, B., *Science 232*:341-347 (1986); Wade, J.D. *et al.*, *Biopolymers 25*:S21-S37 (1986); Fields, G.B., *Int. J. Peptide Prot. Res. 35*:161 (1990); MilliGen Report Nos. 2 and 2a, Millipore Corporation, Bedford, MA, 1987). For example, the more classical method, "tBoc method," or the more recent improved "F-moc" technique may be used (Atherton, E. *et al.*, *J. Chem. Soc. Perkin Trans. I*:538-546 (1981)).

In addition to their uses as inhibitory agents, as disclosed for the protein mutants, these peptides are also used in laboratory tests such as novel elastase titration assays. The peptides are also used to immunize animals to make mutant-specific antibodies, as antigens in immunoassays to screen hybridoma supernatants, or as solid phase immunoadsorbents to purify mutant-specific antibodies.

Production of PAI-1 Mutants by Expression and Purification of Recombinant PAI-1 in *E. coli*

The following methods are preferred and do not represent the exclusive means for carrying out this invention. Techniques for synthesizing oligonucleotides probes are well known in the art and disclosed by, for example, Wu, R., *et al.*, *Prog. Nucl. Acid. Res. Molec. Biol. 21*:101-141 (1978) or Gait, ed., *Oligonucleotide Synthesis* (Current Edition)). Procedures for constructing and

expressing recombinant molecules in accordance with this invention, including appropriate promoters and other control elements, selection markers, *etc.*, are disclosed by Sambrook, J. *et al.*, In: *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Press, Cold Spring Harbor, NY (1989); Ausubel, F.M. *et al. Current Protocols in Molecular Biology*, Vol. 2, Wiley-Interscience, New York, 1987; *DNA Cloning: A Practical Approach*, vol. I & II (D. Glover, ed.), which references are herein incorporated by reference.

Included in this invention is the DNA encoding the PAI-1 mutant, which is preferably a cDNA having the appropriate nucleotide sequence substitutions to encode the mutant proteins as disclosed herein. Such molecules are prepared using conventional methods. Also included herein are prokaryotic or eukaryotic host cells transformed or transfected with a vector comprising the above DNA molecule. Again, the method used for transferring the DNA, expressing the DNA and growing the host cells are well-known in the art and described in the references cited above. Eukaryotic host cells are preferably mammalian cells of an established cell line, although insect cells or plant cells are also contemplated. Appropriate vectors such as viruses, vector sequences, control sequences, such as promoters appropriate for the species of host cells, are conventional and well-known to those skilled in the art and are therefore not described in particular detail herein. In addition to sense DNA, antisense DNA and antisense RNA molecules to the mutant PAI-1 coding sequence are provided herein. Also included is an RNA molecule encoding the PAI-1 mutant.

Site directed Mutagenesis of PAI-1

A preferred method for producing PAI-1 mutants utilizes a commercially available kit and was described by one of the present inventors and his colleagues in a reference which is hereby incorporated by reference in its entirety (Lawrence, D.A. *et al.*, *Biochemistry* 33:3643-3648, 1994).

Site-specific or site-directed mutagenesis allows the production of peptide variants through the use of specific oligonucleotide sequences that encode the DNA sequence of the desired mutation plus a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being

traversed. Typically, a primer of about 20 to 30 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered. The technique of site-directed mutagenesis is well known in the art, as exemplified by publications such as Adelman *et al.*, *DNA* 2:183 (1983), which is incorporated herein by reference. As will be appreciated, the mutagenesis technique typically employs a phage vector that exists in both a single-stranded and double-stranded form. Typical vectors useful in site-directed mutagenesis the M13 phage (Messing *et al.*, *Third Cleveland Symposium on Macromolecules and Recombinant DNA*, Editor A. Walton, Elsevier, Amsterdam (1981)). These phage are commercially available and their use is well known to those skilled in the art. Alternatively, plasmid vectors that contain a single-stranded phage origin of replication (*e.g.*, Veira *et al.*, *Meth. Enzymol. 153*:3 (1987)) may be employed to obtain single-stranded DNA.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector that includes within its sequence a DNA sequence that encodes the PAI-1 protein (or peptide). An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically (*e.g.*, Crea *et al.*, *Proc. Natl. Acad. Sci. (USA) 75*:5765 (1978). This primer is annealed with the vector comprising the single-stranded protein-coding sequence and is subjected to DNA-polymerizing enzymes such as *E. coli* polymerase I Klenow fragment to complete the synthesis of the mutation-bearing strand. Thus, a mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells (such as JM101 cells) and clones are selected that include recombinant vectors bearing the mutated sequence arrangement.

After such a clone is selected, the mutated protein region may be removed and placed in an appropriate vector for protein production, generally an expression vector of the type that may be employed for transformation of an appropriate host.

For producing PAI-1 mutants, the mutagenesis is most preferably performed using the Altered Sites mutagenesis kit (now designated "Altered Sites II®") following the manufacturers instructions (Promega). Briefly, PAI-1 cDNA, along with T7 promoter and terminator regulatory sequences, is isolated as an

XbaI-EcoRV fragment from the PAI-1 expression plasmid pET3aPAI-1 (Sherman *et al.* 1992, *supra*). This fragment is ligated to PstI/XbaI cut pSELECT-1® (Promega) (now designated "pALTER®"), that had been blunt-ended at the PstI site, creating phagemid pSELPAI-1. This construct is then transformed into *E. coli* strain JM109, and single-stranded DNA is produced by infection with the helper phage R408 (Promega).

The following is a list of oligonucleotides used to generate the preferred mutants at the P1 and P4 sites of PAI-1.

P1 Ala	5'-GTCTCAGCCGCCATGGCCCCC	(SEQ ID NO:5)
P1 Val	5'-GTCTCAGCCGTCATGGCCCCC	(SEQ ID NO:6)
P4 Ala	5'-GCTGTCATAGCCTCAGCCCGC	(SEQ ID NO:7)
P4 Ala, P1 Val	5'-GCTGTCATAGCCTCAGCCGTCATGGCCCCC	(SEQ ID NO:8)
P4 Ala, P1 Ala	5'-GCTGTCATAGCCTCAGCCGCCATGGCCCCC	(SEQ ID NO:9)

A newer method is available for enhanced site-elimination mutagenesis which can be applied in the preparation of the mutant PAI-1 proteins . The new Chameleon™ mutagenesis kit (Stratagene) may be used to produce one or more site-specific mutation in virtually any double-stranded plasmid (containing a unique nonessential restriction site), thus eliminating the need for subcloning into M13-based vectors and single-strand DNA rescue (Papworth *et al.*, *Strategies* 7:38-40(1994)). The Chameleon™ kit applies a modification of the unique site-elimination mutagenesis procedure of Deng and Nickoloff (*Anal. Biochem.* 200:81 (1992)). The improved protocol includes the use of: (1) more target DNA and a new primer:template ratio; (2) native T7 DNA polymerase instead of T4 DNA polymerase; (3) a new *mut*S cell line that does not produce endonuclease A; and (4) highly competent XL*mut*S and XL1-Blue® cells for transformation of mutated plasmid DNA. These modifications increase the yield and quality of mutated plasmid DNA, resulting in consistently higher colony numbers and mutagenesis efficiencies. The Chameleon™ mutagenesis kit has been used to introduce insertions, point mutations and deletions as large as 48 bp (Papworth *et al.*, *Strategies* 7:78-79 (1994)) and has also been used with three mutagenic oligonucleotides to simultaneously generate triple mutations. The kit includes competent cells of the XL*mut*S host strain bearing the *endA* mutation which

removes an endonuclease that degrades miniprep DNA, improving the yield and quality of the mutated plasmid DNA and the reproducibility of the mutagenesis procedure.

The mutagenesis procedure involves simultaneously annealing two oligonucleotide primers to the same strand of denatured double-stranded plasmid DNA. One primer (the mutagenic primer) introduces a chosen mutation, and the second primer (the selection primer) alters the sequence of a unique restriction site in the plasmid in order to create a new restriction site. Extension of these primers with T7 polymerase and ligation of the resulting molecules with T4 ligase are followed by restriction enzyme digestion. Any plasmid molecules that renature without inclusion of the selection primer will be linearized, while those that form with the selection primer will not. The resulting mixture is transformed into the highly competent XL*mut*S E. *coli* strain, which is unable to perform mismatch repair. The transformed bacteria are grown overnight in liquid culture, and the plasmid DNA is recovered and treated again with the restriction enzyme that digests plasmids containing the original restriction site. Plasmids containing the new restriction site and the chosen mutation will resist digestion. Transformation of this DNA into highly competent E. *coli* such as XL1-Blue results in 70-91% of the colonies containing mutated plasmids. If a second round of mutagenesis is desired, a switch primer can be used to "switch" from the new unique restriction site back to the original or another restriction site, at the same time incorporating another mutation. This process makes it possible to perform several rounds of mutation.

Selection primers made by Stratagene select against restriction enzyme sites in the antibiotic-resistance genes for ampicillin, chloramphenicol and neomycin/kanamycin. (There are also primers available for the ColE1 origin of replication and the polylinker of both SK and KS versions of the pBluescript® II phagemid.) The switch primers allow a second round of mutagenesis to recreate the original unique restriction site.

Expression, Purification and Characterization of PAI-1 Mutants

A novel phagemid vector for efficient mutagenesis and protein expression has been designed by one of the present inventors and his colleagues. This

construct, pSELPAI-1, eliminates the need to isolate and subclone each new mutant into an expression plasmid. The inclusion of T7 promoter and terminator sequences in the pSELPAI-1 constructs permits efficient PAI-1 expression directly from this vector using an *E. coli* strain producing T7 polymerase (Studier *et al.*, 1990, *Meth. Enzymol. 185*:60-89). Using this system, site-directed mutagenesis is generally achieved with greater than 50% efficiency. In addition, sequence analysis of greater than 10kb, from 8 independent clones, has identified no other mutations, indicating a very low rate of secondary mutations (<0.01%).

Briefly cells of the *E. coli* strain BL21 (DE3) transformed with the pSELPAI-1 mutants are grown to an OD_{650} of 0.5. PAI-1 production is induced by the addition of 1M isopropylthio-β-D-galactoside, and growth is continued at 37°C for 2h. Cells are harvested and PAI-1 is purified as described Lawrence *et al.*, 1989, *supra;* Sherman *et al.*, 1992, *supra*). Protein yields are approximately 1-5 mg/L of cell culture. Purity is assessed by SDS-PAGE and staining by Coomassie blue. Inhibitory activity against both uPA (American Diagnostica) and tPA (Activase, Genentech) is measured in a single step chromogenic assay as described (Lawrence *et al.*, 1989, *supra*) and compared to wtPAI-1 purified from *E. coli* carrying the expression plasmid pET3aPAI-1 (Sherman *et al.*, 1992, *supra*). Inhibitory activity against elastase is tested as described in Example I, below. Other activities, enhancement of clearance or inhibition of cell migration are tested using methods described in more detail in the Examples.

All the mutant proteins have specific activities similar to wild type PAI-1, demonstrating approximately 50 % of the calculated maximum theoretical specific activity (Lawrence *et al.*, 1989, *supra*). The chromatographic profiles of each mutant, from every step of the purification, are similar to those of wtPAI-1. None of the mutations significantly affect heparin binding. Each mutant binds Vn with approximately the same affinity as does wtPAI-1.

CHEMICAL MODIFICATION OF THE PROTEIN

A "chemical derivative" of PAI-1 contains additional chemical moieties not normally a part of the protein. Covalent modifications of the PAI-1 mutant proteins are included within the scope of this invention. Such modifications may be introduced into the molecule by reacting targeted amino acid residues with an

organic derivatizing agent that is capable of reacting with selected side chains or terminal residues. Such derivatized moieties may improve the solubility, absorption, biological half life, and the like. The moieties may alternatively eliminate or attenuate any undesirable side effect of the protein and the like. Moieties capable of mediating such effects are disclosed, for example, in *Remington's Pharmaceutical Sciences*, 16th ed., Mack Publishing Co., Easton, PA (1980). Clearly, any chemical modifications included herein will not substantially alter the advantageous properties of the PAI-1 mutants as described above.

Histidyl residues are derivatized by reaction with diethylprocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0.

Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing α-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3- butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

The specific modification of tyrosyl residues per se has been studied extensively, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizol and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'-N-C-N-R') such as 1-cyclohexyl-3-(2-

morpholinyl-(4-ethyl) carbodiimide or 1- ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T.E. Creighton, *Proteins: Structure and Molecule Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)), acetylation of the N-terminal amine, and, in some instances, amidation of the C-terminal carboxyl groups. Commonly used cross-linking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Patents No. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Among the desired chemical modifications is the labeling of the mutant protein or peptide with a detectable label that permits its use in *in* vivo diagnostic methods or *in* vitro detection methods. A "diagnostically effective" amount of the protein is an amount of detectably labeled protein or peptide which, when administered, is sufficient to enable detection of a site protein binding or deposition or clearance. Use of the protein to detect, for example, thrombosis, fibrin deposition, atherosclerotic plaque or cancer is intended. Generally, the dosage of detectably labeled mutant PAI-1 for diagnosis will vary depending on

considerations such as age, condition, sex, and extent of disease in the patient, contraindications, if any, and other variables, to be adjusted by the diagnostician. Dosage can vary from 0.01μg/kg to 2mg/kg, preferably 0.1μg/kg to 1mg/kg. The term "diagnostically labeled" means that the protein or peptide has attached to it a diagnostically detectable label. There are many different labels and methods of labeling known in the art. Examples of the types of labels which can be used in the present invention include radioactive isotopes, paramagnetic isotopes, and compounds which can be imaged by positron emission tomography (PET). Those of ordinary skill in the art will know of other suitable labels for binding to the proteins or peptides used in the invention, or will be able to ascertain such, using routine experiments. Furthermore, the binding of these labels to the protein is done using standard techniques such as cross-linking, covalent attachment, non-covalent attachment, or complexing.

ANTIBODIES SPECIFIC FOR EPITOPES OF THE MUTANT PROTEIN

The present invention is also directed to an antibody specific for the mutant PAI-1 protein. The antibody is one which recognizes an epitope of the mutant protein not present in the wtPAI-1 protein. Such antibodies are produced by convention means such as immunization of an animal with a mutant protein or a peptide thereof which contains one or more amino acid substitution. Such peptides may be chemically synthesized using conventional methods. Methods of immunization, adjuvants, schedules, etc., are all known in the art. An antiserum produced in this way is tested by any immunochemical or serological assay for binding to the mutant protein as well as to the wt protein. Reactivity for the wt protein can be removed by immunoadsorption of the serum to immobilized wt protein until only reactivity to mutant epitopes remain.

Alternatively, a monoclonal antibody (mAb) is produced specific for epitopes of the mutant PAI-1 by appropriate immunization, cell fusion, growth of hybridoma cells and testing and selection of the supernatant for the desired specificity. Those hybridoma cell lines producing the desired mAb are selected and grown in large quantities. Selection is accomplished by standard immunoassay, such as an enzyme immunoassay (EIA or ELISA) of the culture fluids with the wt

protein and the mutant protein. Alternatively, peptides of the mutant protein including the amino acid substitution or substitutions may be used in the screening assay. A mAb of the invention is one which reacts strongly with a mutant protein or peptide and has little or not detectable reactivity with the wtPAI-1.

The antibody of the invention may be used to detect and quantitate the presence of the PAI-1 mutant protein in a biological sample, such as a body fluid or tissue extract of a subject being treated with the protein. In this way, the treatment protocol can be monitored and levels of the mutant evaluated. Furthermore, the antibody can be used to isolate or purify the mutant protein from a mixture containing the wt protein.

Several standard reference works setting forth methods for making, testing and using the antibodies described above include: Hartlow, E. *et al.*, *Antibodies: A Laboratory Manual*, Cold Spring, Harbor Laboratory Press, Cold Spring Harbor, NY, 1988); Maggio, E. (ed.), *Enzyme Immunoassay*, CRC Press, Boca Raton, FL, 1980; Bizollon, Ch (ed.), *Monoclonal Antibodies and New Trends in Immunoassays*, Elsevier, New York, 1984.). These references are incorporated by reference in their entirety.

THERAPEUTIC COMPOSITIONS AND METHODS

The preferred animal subject of the present invention is a mammal. The invention is particularly useful in the treatment of human subjects. By the term "treating" is intended the administering to subjects of a pharmaceutical composition comprising a PAI-1 mutant protein of this invention for inhibiting elastase or inhibiting Vn-dependent cell migration and subsequent proliferation, which inhibition may prevent, ameliorate or cure any of a number of diseases described herein.

The pharmaceutical compositions of the present invention wherein a PAI-1 mutant protein is combined with pharmaceutically acceptable excipient or carrier, may be administered by any means that achieve their intended purpose. Amounts and regimens for the administration of can be determined readily by those with ordinary skill in the clinical art of treating any of the particular diseases. Preferred amounts are described below.

Administration may be by parenteral, subcutaneous (sc), intravenous (iv), intramuscular, intraperitoneal, transdermal, topical or inhalation routes. Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

Compositions within the scope of this invention include all compositions wherein the mutant PAI-1 protein or peptide is contained in an amount effective to achieve its intended purpose. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages comprise 0.1 to 100 mg/kg/body weight, though more preferred dosages are described for certain particular uses, below.

As stated above, in addition to the pharmacologically active protein, the new pharmaceutical preparations may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically as is well known in the art. Suitable solutions for administration by injection or orally, may contain from about 0.01 to 99 percent, active compound(s) together with the excipient.

Included in the scope of this invention are salts of the PAI-1 protein or peptide. The term "salts" refers to both salts of carboxyl groups and to acid addition salts of amino groups of the protein or peptide. Salts of a carboxyl group include inorganic salts, for example, sodium, calcium, ammonium, ferric or zinc salts, and the like, and salts with organic bases such as those formed with amines, such as triethanolamine, arginine, or lysine, piperidine, procaine, and the like. Acid addition salts include salts with mineral acids such as hydrochloric or sulfuric acid, and salts with organic acids such as acetic or oxalic acid.

The pharmaceutical preparations of the present invention are manufactured in a manner which is itself known, for example, by means of conventional mixing, granulating, dissolving, or lyophilizing processes. Suitable excipients may include fillers binders, disintegrating agents, auxiliaries and stabilizers, all of which are known in the art. Suitable formulations for parenteral administration include

aqueous solutions of the proteins in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions that may contain substances which increase the viscosity of the suspension.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral or topical administration, and all three types of formulation may be used simultaneously to achieve systemic administration of the active ingredient.

As described for lung instillation, aerosolized solutions are used. In a sprayable aerosol preparations, the active protein may be in combination with a solid or liquid inert carrier material. This may also be packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant. The aerosol preparations can contain solvents, buffers, surfactants, and antioxidants in addition to the protein of the invention.

For topical application, the proteins of the present invention may be incorporated into topically applied vehicles such as salves or ointments, which have both a soothing effect on the skin as well as a means for administering the active ingredient directly to the affected area.

The carrier for the active ingredient may be either in sprayable or nonsprayable form. Non-sprayable forms can be semi-solid or solid forms comprising a carrier indigenous to topical application and having a dynamic viscosity preferably greater than that of water. Suitable formulations include, but are not limited to, solution, suspensions, emulsions, creams, ointments, powders, liniments, salves, and the like. If desired, these may be sterilized or mixed with auxiliary agents, e.g., preservatives, stabilizers, wetting agents, buffers, or salts for influencing osmotic pressure and the like. Examples of preferred vehicles for non-sprayable topical preparations include ointment bases, e.g., polyethylene glycol-1000 (PEG-1000); conventional creams such as HEB cream; gels; as well as petroleum jelly and the like. One particularly preferred cream is described below.

Other pharmaceutically acceptable carriers for the PAI-1 protein according to the present invention are liposomes, pharmaceutical compositions in which the active protein is contained either dispersed or variously present in corpuscles consisting of aqueous concentric layers adherent to lipidic layers. The active protein is preferably present in the aqueous layer and in the lipidic layer, inside or outside, or, in any event, in the non-homogeneous system generally known as a liposomic suspension. The hydrophobic layer, or lipidic layer, generally, but not exclusively, comprises phospholipids such as lecithin and sphingomyelin, steroids such as cholesterol, more or less ionic surface active substances such as dicetylphosphate, stearylamine or phosphatidic acid, and/or other materials of a hydrophobic nature.

The PAI-1 mutant proteins described herein have been designed specifically to inhibit elastase and to inhibit cell migration, in particular migration of smooth muscle cells (SMCs). Therefore, pharmaceutical compositions comprising such a protein are useful for inhibiting elastase and/or inhibiting cell migration, in the treatment of various diseases and conditions which are associated with elastase activity or undesired cell migration and proliferation.

LUNG DISEASES ASSOCIATED WITH ELASTASE

Elastase is known to play a significant role in a number of inflammatory conditions and other forms of lung injury, and which result in acute respiratory distress syndrome (ARDS) both of the adult variety and the neonatal form (Koleff, M.H. *et al., New Eng. J. Med. 332*:27-37 (1995); Speer, C.P. *et al. Pediatrics 91*:794-799 (1993)). There are currently no useful pharmacotherapeutic approaches to ARDS, particularly early in the disease process. It is believed that a protease-inhibitor imbalance may contribute essentially to acute lung damage in early stages of ARDS. The mutant PAI-1 proteins are useful in restoring this imbalance and tipping it in favor of proteinase (particularly elastase) inhibition.

Furthermore the importance in lung injury of the extravasation of neutrophils from the pulmonary microvascular compartment into interstitium and alveolar space is recognized (Strieter, R.M. *et al., J. Invest. Med. 42*:640- (1994)). These processes involve β2 integrins and selectins, such neutrophil L-selectin interacting with activated endothelium E- and P-selectins and neutrophil β2 integrin interacting with EC ICAM-1 in neutrophil-EC adhesion, margination or

rolling. Expression of these cell surface molecules and the activity of the cells are influenced by the cytokines TNF and IL1. These two cytokines are initiators and promoters, setting into motion cascade of events leading to microvascular inflammation. The mutant PAI-1 proteins are useful in modulating such neutrophil migratory activity and ultimately, in inhibiting the action of their secreted product, elastase which is responsible for much of the tissue injury.

Emphysema is known to be in large part a result of elastase-mediated tissue injury. Augmentation of lung antiprotease levels would be an important therapeutic intervention in prevention or retardation of development of emphysema (Smith, R.M. *et al.*, *J. Clin. Invest.* 84:1145-1154 (1989)). In the foregoing study, aerosols of α1AT were administered to lungs of dogs and sheep. α1AT was found on the surface of alveoli and distal bronchioles 2 hrs after administration and was present in lavage fluid; antielastase activity was proportional to the concentration of human α1AT given.

Emphysema secondary to congenital α1AT deficiency also results from insufficient amounts of α1AT to protect lower respiratory tract from neutrophil elastase (Hubbard, R.C. *et al.*, *J. Clin. Invest.* 84:1349-1354 (1989).

Emphysema, including that due to α1AT deficiency can benefit from treatment with the elastase-inhibiting PAI-1 mutants of the present invention.

In cystic fibrosis, CF, neutrophil-dominated inflammation on respiratory epithelial surface results in chronic epithelial burden of neutrophil elastase (McElvaney, N.G. *et al.*, *Lancet* 337:392-394 (1991)). α1AT given in aerosol form to CF patients suppressed neutrophil elastase in the respiratory epithelial lining fluid (ELF) and restored ELF anti-elastase capacity. This treatment also reversed inhibitory effect of CF ELF on Pseudomonas killing by neutrophils suggesting augmentation of host defenses. Airway inflammation in CF was diminished and IL-8 levels on the respiratory epithelial surface were suppressed by aerosolization of recombinant secretory leukoprotease inhibitor (rSLPI) (McElvaney, N.G. *et al.*, *J. Clin. Invest.* *90*:1296-1301 (1992)). This treatment elastase detectable in ELF and appeared to breaks the cycle of inflammation on CF epithelial surface. rSLPI is a 12kDa single chain nonglycosylated protein made in

E. coli with identical structure and function to normal human SLPI (Thompson, R.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 83:6692-6696 (1986)).

Based on the foregoing, the PAI-1 mutant compositions are used to inhibit elastase in patients with CF, thereby treating various symptoms of the disease.

For treating the above forms of lung disease, use of aerosols is preferred to maintain protective alveolar levels. Those of skill in the art will know how to determine the efficiency of for delivery into alveolus. If efficiency is expected to be in the range of 10-20%, 10-200 mg of active PAI-1 mutant protein will be needed to be aerosolized per day or 70-1400 mg/week to maintain desired levels in alveolar fluid. improved aerosol delivery methods would reduce amount required. Aerosolized PAI-1 mutant proteins retain their antielastase activity and can penetrate into and deposit on the surface of distal airspaces in lung. Aerosolized PAI-1 mutant proteins in avoids problems with high renal clearance associated with intravenous (iv) administration of some agents.

Aerosol is generated by convention means, for example with compressed air-driven nebulizer. The aerosol preferably has mass median diameter of 1-4μM. Escalating dosing may be used and the amounts of PAI-1 proteins can be evaluated by lavage and the dosing adjusted accordingly.

Alternatively, the proteins can be administered parenterally at a dose range of about 10-200 mg/kg/wk.

OTHER ELASTASE-RELATED DISEASES

According to Travis, J. *et al.*, *J. Respir. Crit. Care Med,* 150:S143-146 (1994), periodontal disease shares certain pathophysiologic features with emphysema such as accumulation and degranulation of neutrophils at inflammatory sites as result of frustrated phagocytosis and specific activation of these phagocytic cells. In periodontitis, the process begins with accumulation of plaque at base of teeth followed by growth of opportunistic anaerobic bacterial below the gum line. These organisms resist killing by both monocytes and neutrophils, secrete proteinases that activate kallikrein-kinin pathway, degrade clotting factors and release chemotactic factor C5a from complement. Neutrophils are recruited to infected sites, attempt to phagocytose bacteria, followed by inactivation of proteinase inhibitors and degradation of connective tissue proteins, yielding

destruction of gingiva. The present compositions are useful in treating periodontal disease, topically or systemically, through inhibition of elastase and other mechanisms discussed above.

Atopic dermatitis (AD), which affects both children and adults, has no established etiology though it has been suggested that during inflammation, an excess of serine proteinases accumulates at the local site of injury together with a deficiency of their natural inhibitors (Wachter, A.M. *et al.*, *Ann. Allergy, 69*:407-414 (1992)). α1AT was tested for treatment of recalcitrant AD. Patients showed significant clinical improvement within 6 to 21 days of initiation of alternate day therapy. α1AT stopped pain, pruritus and promoted tissue healing without scarring.

Periodontal disease is treated preferably by topical application of the mutant PAI-1 protein, or alternatively, by systemic therapy. AD is treated by topical administration of a PAI-1 mutant protein. Effective doses for both diseases range from about 1 to about 100mg/ml, preferably about 20-50 mg/ml of mutant PAI-1 protein in aqueous solution given on an alternate days schedule. For treating hands, about 5-10 ml the protein in solution is introduced into an occlusive glove which is placed on the subject. Other known occlusive dressings may be used at other sites. In conjunction with the aqueous solution, a cream of PAI-1 mutant protein at a concentration of about 0.2-5%, preferably about 1% is used. For example, aqueous treatment is given on alternate days for 2 hrs followed by topical application of the cream This is repeated 3 times during day. At night, continuous 8 hr application of the aqueous protein is administered in an occlusive dressing. Alternate day therapy is the cream applied thrice per day. At later stages of treatment, a maintenance dose of about 1-8% cream, preferably about 5% is given. This therapy may be combined with topical steroids. Maintenance therapy may be give for weeks to months, depending on the patients' response. A preferred emollient cream base is petroleum, mineral oil, mineral wax and alcohol (Aquaphor; Beiersdorf, Inc.) though other compositions known in the art may be used. Formulation is done using conventional methods.

Evidence exists for a T lymphocyte protein receptor with elastase-like character to participate in fusion of HIV-1 with permissive host cells (Bristow,

C.L. *et al.*, *International Immunol.* 7:239-249 (1995)). A synthetic elastase inhibitor (MAAPVCK: methoxysuccinyl-Ala-Ala-Pro-Val-chloromethylketone) significantly reduced HIV infectivity when present during contact between virus and cells. The human T cell elastase-like homolog is membrane-associated and is protected from bystander proteolysis by association with its natural inhibitor, α1PI. Evidence suggests ligand exchange between gp41-gp120-CD4 complexes and elastase-like protease-α1PI complexes. Complexes between gp120 and CD4 may induce dissociation of elastase ant α1AT, and disruption of the latter complexes may explain ability of MAAPVCK to interfere in HIV infectivity. Blocking the catalytic site of elastase-like protease would preempt HIV fusion. Therefore the compositions of the present invention are useful to target such complexes, inhibit the elastase-like activity, and thereby contribute to the antiviral effect on HIV.

ATHEROSCLEROSIS, RESTENOSIS AND VASCULAR DISEASE

Atherosclerosis and the formation of neointima in blood vessels, especially in arteries, is stimulated by a number of events, including platelet activation leading to thrombosis and secretion growth factors, as well as stimulation of SMC migration and proliferation resulting in neointima formation (see, for example, Reidy, M.A. *et al.*, *Circulation* 86III:43,46 (1992); Jackson, C.L. *et al.*, *Arterioscler. Thromb.* 13:1218-1226; Matsuno, H. *et al.*, *Nippon Yakurigaku Zasshi 106*:143-155 (1995)). Peptides containing the RGD sequence, chief among them Vn, can prevent the binding of several integrins including $\alpha_v\beta3$ in SMC migration. By inhibiting integrin function, particularly the binding of $\alpha_v\beta3$ (also referred herein to as Vn receptor or VnR), the formation of neotintima is inhibited as a consequence of lowering the percentage SMC migrating into and proliferating in the vascular media and neointima. The PAI-1 mutant proteins of the present invention, by blocking integrin interaction with Vn, are useful in reduction of thrombus and neointima formation, thereby preventing the generation of atherosclerosis.

Restenosis, the narrowing that occurs in certain patients as a result of neointimal SMC accumulation after balloon angioplasty as a treatment for end-stage atherosclerosis, is an important long term complication. Its incidence is about 30 to 50% within six months post-angioplasty (Libby, P. *et al. Circulation 86*:III 47-52 (1992); Groves, P.H. *et al. Atheroscler. 117*:83-96 (1995); Nikol, S., *Wien Klin*

Wochenschr. *107*:379-89 (1995). From animal models it is known that restenosis takes place in several phases: thrombosis, inflammation, cell-proliferation and matrix formation. The process is complex, with various factors interacting in each phase as agonists or antagonists. After more than 15 years experience in balloon angioplasty, there is an urgent need to develop therapeutic strategies based on currently available information. A number of approaches have been suggested, including selective elimination or alteration of proliferating cells, enhancement of natural growth inhibitors, blocking of signal transduction or inhibition of the gene expression for distinct growth stimulating proteins. The present invention provides a specific approach directed at disrupting the adhesion, migration and subsequent proliferation of SMC in the vasculature by providing a PAI-1 mutant capable of inhibiting these steps by binding to Vn and disrupting Vn interactions with its integrin receptors on cells.

Groves *et al.*, *supra* described a quantitative pig carotid artery model which can be used in the evaluation of the present mutant PAI-1 compositions and which reflects two distinct kinds of injury which occur in human disease: medial dilation and deep medial tearing with rupture of the internal elastic lamina. In this model, the time course of neointima formation is evaluated morophometrically and SMC proliferation is measured by immunocytochemical detection of the "proliferating cell nuclear antigen" (PCNA) at various times after balloon injury. In this model, dilatation injury causes medial enlargement and neointima formation by 7 days, as does rupture of the internal elastic lamina. Balloon injury increases the PCNA index of SMCs in the media underlying an intact internal elastic lamina maximally after three days, and in the neointima and in the neomedia after 7 days.

A recently described improved model of human restenosis in monkeys utilizes atherosclerotic monkeys fed an atherogenic diet for 36 months (Geary, R.L. *et al.*, *Arterioscler Thromb. Vasc. Biol.* *16*:34-43 (1996). Angioplasty is performed in one iliac artery. At varying time points (up to 28 days), proliferating cells are enumerated using bromodeoxyuridine labeling and arteries may be fixed *in situ* for examination. It has been observed that angioplasty often fractures the intimal plaque and media, transiently increasing the lumen caliber and artery sizes, which commonly returns to baseline by 7 days. Proliferation was increased throughout the artery wall at 4 and 7 days and declined later to control rates. The intima thickened markedly from 14 to 28

days. This response to angioplasty closely resembles that in humans. PAI-1 mutants according to this invention are given to monkeys in conjunction with the angioplasty to evaluate dose and administration regimens. The results may be applied directly to human subjects or other mammalian species.

Libby *et al.*, *supra*, discussed restenosis mechanisms based on a cytokine/growth factor cascade following angioplasty. Acute local thrombosis and/or mechanical injury triggers cytokine/growth factor gene expression by resident macrophages and SMCs which evokes a secondary growth factor and cytokine response that could amplify and sustain the proliferative response. Human atheromas contain variable numbers of macrophages. The variability in macrophage content of atheromas which may determine the propensity to develop restenosis could explain why all lesions do not restenose. In the context of these mechanisms, the PAI-1 mutant proteins, by inhibiting Vn-dependent SMC migration, would prevent or reduce the deranged behavior of SMCs during restenosis triggered by vascular injury.

Studies with transgenic mice over- or under-expressing components of the fibrinolytic system revealed a significant role in fibrin clot surveillance, reproduction, vascular wound healing, brain function, health and survival (Carmeliet, P.F., *Baillieres Clin Haematol* 8:391-401 (1995)). Over time, both types of PAs appear to have evolved with specific yet overlapping biological properties. Loss of PA gene function is thought to be important in atherosclerosis, neoangiogenesis, inflammatory lung and kidney disease and malignancy. The PA knockout mice with their thrombotic phenotypes allowed study of the restoration of normal thrombolytic function and prevent thrombosis by gene transfer of wild type or mutant PA genes. Impaired thrombolysis of tPA-deficient mice was restored using viral-mediated gene transfer of recombinant tPA. Analysis of neointima formation in PA-deficient mice suggested that controlled reduction of fibrinolytic activity in the vessel wall might be beneficial for prevention or reduction of restenosis. This model permits evaluation of the present PAI-1 mutants, either by gene transfer or exogenous therapy, in preventing fibrinolytic processes as well as inhibiting cell migration as discovered by the present inventors.

Sawa, H. *et al.*, *J. Am. Coll. Cardiol* 24:1742-1748 (1994), examined rabbit carotid arteries to test whether altered gene expression of PAI-1 occurred within the arterial wall after experimental balloon injury. Balloon injury (as a model for

angioplasty) induced intramural PAI-1 expression (mRNA and protein) in vascular SMCs and ECs. The decreased cell surface fibrinolytic activity likely to result from the increased PAI-1 expression may initiate or exacerbate mural thrombosis. As a consequence, excessive stimulation with clot-associated mitogens may stimulate vascular SMC proliferation, which, coupled with increased accumulation of ECM attributable to a decreased plasma-mediated degradation, may contribute to restenosis.

The present invention provides a means to avoid or prevent the aforementioned events which involve PAI-1 in the pathogenetic process. By providing to a subject a PAI-1 mutant with high affinity for Vn, the Vn-dependent migration of SMCs is reduced or prevented, thereby avoiding the subsequent proliferation which contributes to the restenosis.

CANCER, ANGIOGENESIS AND FIBROSIS

Work by Cheresh and colleagues has provided an insight into the various types of VnR integrins and their role in various biological reactions of clinical importance. Of particular importance to the present therapeutic methods are the interactions between the VnR $\alpha_V\beta_3$ and Vn, which are inhibitable by various of the PAI-1 mutants of this invention. By preventing interaction of these adhesion molecules, the important process of cell migration can be diminished or halted, with a number of important consequences for those diseases and conditions associated with undesirable cell migration, which leads to proliferation and pathogenesis. In addition to the vascular phenomena and diseases discussed above, such migration is important in tumor invasion and metastasis, which can be suppressed by the present compositions and methods. Furthermore, as detailed below, angiogenesis and neovascularization is dependent upon intact VnR-Vn interactions. Thus, disruption of cell binding to Vn by PAI-1 mutants will inhibit angiogenesis, an effect which can be harnessed to inhibit both local and metastatic tumor growth.

Homologous integrins with identical α subunits and structurally distinct β subunits result in different functional recognition repertoires among various cell types. For example, carcinoma cells were described as expressing an novel VnR integrin ($\alpha_V\beta_x$) which mediated cell adhesion to Vn, but not to fibrinogen or von Willebrand factor (Cheresh, D.A. *et al., Cell 57*:59-69 (1989)). In contrast, melanoma and ECs express a VnR ($\alpha_v\beta3$) that promotes cell attachment to all of these matrix components.

The carcinoma cell integrin was composed of an α subunit indistinguishable from the α_V of the VnR and a previously unrecognized β subunit (β_x). These cells also lacked mRNA encoding integrin β_3. This variant receptor mediated cell adhesion to Vn as well as fibronectin based on antibody inhibition studies.

Integrin α chains can complex with more than a single β chain in the same cell (Krissansen, G.W. *et al.*, *J. Biol. Chem.* *265*:823-830 (1990)). Differential regulation of expression of the different β subunits that associate with the VnR α chain may play a role during cell differentiation of monocyte-macrophages.

Important for this invention is the discovery of the requirement for the integrin $\beta3$ subunit for carcinoma cells to spread or migrate on Vn (and fibrinogen) (Leavesley, D.I. *J. Cell Biol.* *117*:1101-1107 (1992)). A human pancreatic carcinoma was found to use integrin $\alpha_v\beta5$ as its primary VnR as it failed to express $\alpha_V\beta_3$. These cells could not form focal contacts, spread or migrate on Vn but readily did so on collagen in a β_1 integrin-dependent manner. Transfection of these cancer cells with cDNA encoding the integrin β_3 subunit caused surface expression of a functional $\alpha_V\beta_3$ heterodimer providing these cells with novel adhesive and biological properties, namely the capacity to attach and spread on Vn or fibrinogen with β_3 localization to focal contacts. These cells gained the capacity to migrate through a porous membrane in response to either Vn or fibrinogen. These results demonstrated that the β_3 and β_5 integrin subunits, when associated with α_V, promote distinct cellular responses to a Vn extracellular environment. According to this invention, all of the foregoing interactions between tumor cells and ECM are inhibitable by the PAI-1 mutants.

It is important to note that several different integrins are present on the same cells (e.g., $\alpha_V\beta_1$, $\alpha_V\beta_3$ and $\alpha_v\beta_5$. However, it is the β_3 chain which is upregulated when cells are about to migrate. Nevertheless, any cell which utilizes any integrin to bind to the RGD site of Vn will be inhibited in this interaction and in its subsequent migration by the PAI-1 mutants described herein.

The requirement for vascular integrin $\alpha_V\beta_3$ for angiogenesis was shown by Brooks, P.C. *et al.*, *Science* 264:569-571 1994). This VnR was expressed on blood vessels in wound granulation tissue and increased in expression during angiogenesis. An antibody to $\alpha_V\beta_3$ blocked angiogenesis induced by cytokines, growth factors and fragments of melanoma tumor. This identifies $\alpha_V\beta_3$ as a therapeutic target for diseases

characterized by neovascularization. The present invention provides a therapeutic composition and method aimed at this target: PAI-1 mutants which are designed to inhibit migration and which maintain high affinity for Vn. Administration of effective amounts of these compositions will disrupt the molecular interactions required for angiogenesis. It is preferred to administer the compositions to the affected tissue, for example by intralesional injection into tumors, or by specific targeting using targeted liposomes.

Wound healing requires a coordinated influx of fibroblasts, vascular endothelium and epithelium. Agents which promote a more rapid influx of fibroblasts, endothelial and epithelial cells into wounds should increase the rate at which wounds heal. However, such stimulation may also result in unwanted tissue fibrosis and scarring. The PAI-1 mutants of the present invention preferably applied topically are useful in downregulating the influx of, for example, fibroblasts into a wound. Judicious use of these proteins will allow a balance to be achieved between wound healing and fibrosis or scarring.

Fibrosis in the lung is a major problem in chemotherapy with agents such as bleomycin and adriamycin. Fibroblasts migrate into the lung tissue (or other chronically inflamed tissue) on a fibrin matrix and lay down collagen. Endogenous PAI-1 bound to the fibrin matrix is displaced to allow these processes. Knockout mice overexpressing PAI-1 showed inhibition of lung fibrosis in response to bleomycin (Eitzman, D.T. *et al., J. Clin. Invest.* 97:232-237 (1996)). Pathogenesis of lung fibrosis as well as fibrosis in other chronically inflamed tissues involves increases in tissue factor which stimulates prothrombin activation to thrombin which results in fibrinogen conversion to fibrin and fibrin deposition. Inflammation also upregulates PAI-1. However, cells such as fibroblasts are able to displace PAI-1 in binding to and migrating along the fibrin matrix. Ultimately, their migration and secretion of collagen results in fibrosis. The PAI-1 mutant protein of this invention are used to disrupt this process by inhibiting the cell:matrix interaction and inhibiting fibroblast migration and generation of fibrosis in the lung or any other chronically inflamed tissue. The protein may be administered as an aerosol or by systemic injection or both. Alternatively, the protein may be targeted to a specific tissue by liposome carriers or other means known in the art for targeted drug delivery.

THROMBOSIS

Mutant PAI-1 proteins also serve as improved thrombin inhibitors. Thrombin bind to fibrin in a clot is protected from inhibition by normal thrombin inhibitors. The mutant PAI-1 proteins are able to inhibit such "protected" thrombin on surfaces. In this way, the mutant PAI-1 compositions are used to treat deep venous thrombosis, where clot-bound thrombin serves to promote extension of the clot leading to blockage and myocardial infarction, for example Clot extension is resistant to traditional anticoagulant therapy. Administration of PAI-1 mutant protein will clear thrombin from a clot and thereby prevent clot extension and its pathologic sequelae.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

EXAMPLE I

Inhibition of Elastase by PAI-1 Mutants

Studies were performed to test the ability of PAI-1 mutants to bind to elastase in a manner which permitted inhibition elastase enzymatic activity. Also tested was the ability of the PAI-1 mutant to stimulate endocytosis of elastase the dependence of this internalization on LDL-like receptor proteins.

Assay for Elastase Activity and its Inhibition

Neutrophil elastase and pancreatic elastase (1μg/ml) were incubated with increasing concentrations of either wtPAI-1 or P1-Ala-PAI-1, or α1AT for 30 min at room temperature in 50mM Tris pH 7.5, 150mM NaCl, 100μg/ml BSA, 0.01% Tween-80 (100μl). The chromogenic substrate Ala-Ala-Ala-pNA (Sigma) (100μl) was added to 1mM final concentration. The change in absorbance at 405nm was measured at 37°C for 30 min., and the rate of change was calculated for the last 15 min.

SDS-PAGE Analysis of Complex Formation between PAI-1 and Elastase

Neutrophil elastase (0.45 mg/ml) and pancreatic elastase (1 mg/ml) was incubated with a 4-fold molar excess of either wild-type PAI-1 (lanes 2 and 4) or P1-Ala-PAI-1 (lanes 3 and 6) for 30 minutes at room temperature and then

samples were electrophoresed on a 12.5 % SDS gel and stained with Coomassie blue.

Endocytosis of ^{125}I-neutrophil elastase by type II pneumocytes

Type II pneumocytes in 12 well plates (0.5-1 x 10^6 cells/well) were washed twice in serum-free medium and incubated for 30 min in serum-free medium + 1.5% BSA. ^{125}I-elastase from neutrophils (5nM) was added to each group in the presence or absence of 1mM of the receptor associated protein ("RAP") which inhibits binding of all ligands to the LDL-receptor-related protein (LRP). Cells were incubated for 30 min at 37°C before the P1 Ala PAI-1 mutant or α1AT ("α1") (25 nM) were added to the wells. Cells were incubated for 4 hours at 37°C. Wells were washed twice using PBS and incubated for 5 min in serum-free medium containing 0.5 mg/ml trypsin and proteinase K and 0.5 mM EDTA. Cells were centrifuged and the radioactivity in the cell pellet was counted as a measure of internalized elastase.

Results

Whereas wtPAI-1 did not inhibit pancreatic elastase (Fig. 5), the P1 Ala mutant PAI-1 did, although with less potency than α1AT. As for neutrophil elastase, both wild type and mutant PAI-1 inhibited enzymatic activity, with the mutant showing about four-fold greater inhibitory capacity.

SDS-PAGE (Fig. 6) of mixtures of elastase with wtPAI-1 or P1 Ala PAI-1 showed the presence of the elastase and the inhibitor when wtPAI-1 was used, with no evidence of complex formation. In contrast, P1 Ala PAI-1 formed complexes with the elastase. Doublets indicate cleaved products which are still inhibited.

As for internalization (clearance) of elastase, α1AT did not promote, and even inhibited the internalization. RAP had no effect on this inhibition. In contrast, P1 Ala PAI-1 caused marked increase in elastase internalization, which was sensitive to the LRP inhibitor (Fig. 7). It was concluded that the PAI-1 mutant stimulated endocytosis and uptake of through the LDL-related clearance receptors.

EXAMPLE II

PAI-1 and Vitronectin Promote the Cellular Clearance of Thrombin by LDL-Receptor Related Proteins 1 and 2

(see: Stefansson *et al.*, *J. Biol. Chem.* *271*:8215-8229 (1996 Apr. 5)

The following study evaluated cell-mediated endocytosis as a potential mechanism for regulating levels of extravascular thrombin and determined whether PAI-1, Vn and receptors of the LDLR family have roles in the process.

I. Materials and Methods

Proteins

Human α-thrombin was obtained from Dr. F. Church (University of North Carolina, Chapel Hill, NC) or purchased from Enzyme Research Laboratories (South Bend, IN.). Human HCII was obtained from Dr. F. Church. Human ATIII was obtained from Dr. K. Ingham (American Red Cross, Rockville, MD). Human α_1AT was purchased from Sigma Chemical Co. (St. Louis, MO). Human fibrinogen was purchased from Enzyme Research Laboratories (South Bend, IN). D-phenylalanyl-L-prolyl-L-arginine chloromethyl ketone (PPACK) was purchased from Calbiochem (La Jolla, CA). Human 39 kDa receptor associated protein (RAP) was expressed and purified as described (Williams, S.E., *et al.*, (1992) *J. Biol. Chem.267*: 9035-9040). Low density lipoprotein receptor-related protein (LRP-1) was purified as described (Ashcom, J.D., *et al.*, (1990) *J. Cell. Biol. 110*:1041-1048). Glycoprotein 330/(LRP-2) was purified as previously described (Kounnas, W.S. *et al.*, (1994) *Ann. NY Acad. Sci. 737*:114-124). Native human Vn was provided by Dr. D. Mosher (University of Wisconsin, Madison, WI). Urea denatured human Vn (conformationally altered) was provided by Dr. T. J. Podor (McMaster University, Hamilton, Ontario, Canada). Human uPA was provided by Dr. J. Henkin (Abbott Laboratories, Abbott Park, IL). Bacterially expressed human PAI-1 was purchased from Molecular Innovations (Royal Oak, MI). A mutant form of PAI-1 having a Gln_{123} to Lys substitution that makes it unable to bind to Vn (Lawrence, *et al.*, (1994) *supra*) was prepared as described (Kvassman, J.D. *et al.*, J.D. (1995) *Fibrinolysis* *9*:215-221).

Radioiodination of proteins was performed by using IODO-GEN (Pierce Chemical Co., Rockford, IL). Complexes of thrombin and various inhibitors were

prepared by incubating the ^{125}I-thrombin with each inhibitor at a 2:1 molar ratio for 30 min at 25°C followed by absorption of free thrombin by chromatography on a column ATIII-Sepharose (2 mg ATIII/ml resin). To prepare active site inhibited thrombin, ^{125}I-thrombin (100 nM) was incubated with PPACK (5 mM) for 30 min at 25°C in TBS. The complexes were tested for thrombin activity by incubation with a fibrinogen solution (1 mg fibrinogen/ml in TBS, 5 mM $CaCl_2$) at 25°C for 30 min and assaying for fibrin formation.

Antibodies

The rabbit antisera against LRP-1 (rb777 and rb810), LRP-2 (rb239 or rb784), and a synthetic peptide corresponding to the 11 C-terminal residues of the cytoplasmic domain of LRP-1 (rb704) have been described previously (Kounnas, W.S. *et al.*, (1994) *Ann. NY Acad. Sci.* *737*:114-124; Kounnas, M.Z. *et al.*, (1992) *J. Biol. Chem.* *267*:12420-12423; Strickland, D.K. *et al.*, (1991) *J. Biol. Chem.* *266*:13364-13369). Receptor-specific IgG were selected from the LRP-1 and LRP-2 sera by chromatography on columns of either LRP-1 or LRP-2-Sepharose (1-2 mg receptor/ml resin). Control rabbit IgG was purified from non-immune sera. IgG from each preparation was purified by affinity chromatography on protein G-Sepharose and absorbed on a column of RAP-Sepharose (2 mg RAP/ml resin). Rabbit anti-murine PAI-1 serum was from Molecular Innovations (Royal Oak, MI).

Cells

Rat pre-type II pneumocytes (Mallampalli R.K., *et al.*, (1992) *In Vitro Cell. Dev. Biol.* *28A*:181-187) were grown in Waymouth's media (Gibco) supplemented with 10% bovine calf serum (Hyclone, Logan, UT), penicillin, and streptomycin.

Solid phase binding assays

Solid phase binding assays were performed as described (Williams, S.E., *et al.* (1992) *J. Biol. Chem.* *267*:9035-9040). ^{125}I-thrombin:PAI-1 complexes (1nM) in the presence of increasing concentrations of unlabeled complex or RAP were incubated with microtiter wells coated with LRP-1, LRP-2 or BSA (3μg/ml). The program "Ligand" was used to analyze the competition data and to determine dissociation constants (K_d) for receptor-ligand interactions.

Endocytosis and degradation of thrombin and uPA

Type II pneumocytes were seeded into wells of 12-well plates (1-2.5 x 10^5 cells/well) and grown 18h at 37°C, 5% CO_2 in Waymouth's medium containing 10% bovine calf serum. Before addition of ^{125}I-thrombin:inhibitor complexes, the cells were washed twice in serum-free Waymouth's medium and incubated for 30 min in medium containing 1.5% BSA, 20 mM Hepes pH 7.4, Nutridoma serum-substitute, penicillin, and streptomycin (assay medium). ^{125}I-complexes in assay medium were added to cell layers and incubated for 4-6 h at 37°C. Where indicated, unlabeled thrombin:PAI-1 (800nM), RAP (1μM) or IgG (150μg/ml) were added 30 min prior to addition of ^{125}I-ligand and were kept present during the assay. The quantitation of the amount of endocytosed and degraded ligand were done as described in (Stefansson, S. *et al.*, (1995) *J. Cell Sci. 108*: 2361-2369). Briefly, following the incubation period, the medium was removed from the cells and precipitated with 10% trichloroacetic acid. Soluble radioactivity was taken to represent degraded ligand. Cell layers were washed twice with serum-free medium and incubated in serum free-medium containing trypsin and proteinase K (0.5mg/ml) and 0.5mM EDTA for 2-5 minutes at 4°C. The cells were then centrifuged at 6000 X g for 2 minutes and the radioactivity in the cell pellet was taken to represent the amount of endocytosed ligand.

To evaluate the effects of wild-type and mutant PAI-1 on the clearance (endocytosis and degradation) of exogenously added ^{125}I-thrombin, cells were grown in medium containing 10% serum as described above. Washed monolayers were then incubated either with wild-type PAI-1 (10nM) or mutant PAI-1 (10nM) for 20 min at 37°C. ^{125}I-thrombin (10nM) or ^{125}I-uPA (10nM) was added and incubated for 4-6 h at 37°C. Where indicated, RAP (1μM) was incubated for 30 min prior to addition of the ligands.

To evaluate the effects of native versus conformationally altered Vn on the clearance of exogenously added PAI-1 and active ^{125}I-thrombin, cells were grown in serum-free medium for 18 h at 37°C on tissue culture plates coated with 0.1% gelatin. Medium was removed and assay medium added for 1 h at 37°C to block unoccupied binding sites with BSA. Cell monolayers were incubated with either native (50nM) or conformationally altered Vn (50nM) for 1 h at 37°C. Cell

monolayers were then washed twice with assay medium to remove unbound Vn. Wild-type PAI-1 (10nM) was added and incubated for 1 h at 37°C. ^{125}I-thrombin (10nM) or ^{125}I-uPA (10nM) were added and incubated for 4-6 h at 37°C.

II. Results

The efficient endocytosis and degradation of active thrombin depends on PAI-1.

When the endocytosis and degradation of exogenously added active versus active site-inhibited ^{125}I-thrombin was compared, the active thrombin was more efficiently endocytosed and degraded (Figures 8-9). Considering that the clearance of two other proteinases, tPA and uPA have been shown to be augmented by complex formation with PAI-1, the possibility that PAI-1 was mediating the clearance of the active thrombin in the cultured pre-type II pneumocyte cells was investigated. Pretreatment of cell layers with PAI-1 antibodies resulted in the inhibition of both endocytosis and degradation of active ^{125}I-thrombin whereas control rabbit IgG had a negligible effect on either process (Figures 8-9). These data show that active thrombin is endocytosed and degraded and suggest that PAI-1 is involved.

Thrombin in complex with PAI-1 is more efficiently endocytosed and degraded as compared to complexes with ATIII, HCII or α_1AT

The relative efficiency of cell mediated clearance of ^{125}I-thrombin in complex with various serpins was investigated using the pre-type II pneumocyte cell line. As shown in Figures 10-11, ^{125}I-thrombin:PAI-1 complexes were endocytosed (*panel A*) and degraded (*panel B*) at levels six-fold greater ($n = 2$) than complexes of thrombin and the serpins ATIII, HCII and α_1AT, or of thrombin and the synthetic peptide inhibitor PPACK.

Members of the low density lipoprotein receptor family mediate the endocytosis and degradation of thrombin:PAI-1 complex.

Considering that PAI-1 facilitates the cellular clearance of active uPA via members of the LDLR family, the potential role of these receptors in the clearance of thrombin:PAI-1 with thrombin was studied. The pre-type II pneumocyte cell line was previously shown to express two members of the LDLR family, LRP-1 and LRP-2 (Stefansson, *supra*). As shown in Figures 12-13, antagonists of LRP-1

and LRP-2 function, namely the 39 kDa receptor-associated protein (RAP), and antibodies to either LRP-1 or LRP-2 each inhibited the endocytosis and degradation of ^{125}I-thrombin:PAI-1 complex. The extent of RAP inhibition was similar to that using excess unlabeled thrombin:PAI complex suggesting that members of the LDLR family were mediating the endocytosis and degradation of thrombin:PAI.

The results indicate that at least two members of the LDLR family, LRP-1 and LRP-2 can mediate endocytosis and degradation of ^{125}I-thrombin:PAI-1. The inability of the combination of both LRP antibodies to inhibit endocytosis and degradation to the same extent as did RAP (Figures 12-13) suggests that additional LDLR family expressed by the pre-type II pneumocytes are able to endocytose thrombin:PAI-1.

Thrombin:PAI-1 complex binds LRP-1 and LRP-2 in solid phase assay

Solid phase binding assays using purified components were performed to determine whether thrombin:PAI-1 was able to bind directly to LRP-1 and LRP-2. As shown in Figures 14-15, ^{125}I-thrombin:PAI-1 complex bound to microtiter wells coated with either receptor. By fitting the homologous ligand displacement data to a model of a single class of sites, dissociation constants (K_d) of 3.3nM (n=3) and 13nM (n=2) were derived for the binding of ^{125}I-thrombin:PAI-1 to LRP-1 and LRP-2, respectively. RAP was found to compete for the binding of ^{125}I-complex to both receptors. Thrombin or PAI-1 alone did not compete efficiently for ^{125}I-thrombin:PAI-1 binding to either receptor (K_i's >700nM).

The results indicate that thrombin:PAI-1 complex binds with high affinity to LRP-1 and LRP-2. The fact that PAI-1 binds to both receptors yet is unable to compete for thrombin:PAI-1 binding suggests that the complex possesses an additional receptor binding site not present on either thrombin or PAI-1 alone.

The ability of PAI-1 to bind Vn facilitates the efficient clearance of thrombin

Because Vn had been shown to promote the inhibition of thrombin by PAI-1, studies were done to determine whether such a mechanism was involved in the pre-type II pneumocyte clearance of thrombin. Pre-type II pneumocyte layers grown in serum-containing medium were incubated with either wild-type PAI-1 or

a mutant PAI-1 which is unable to bind Vn but is identical to wild-type PAI-1 in its ability to bind heparin or to inhibit uPA (Lawrence, D.A. *et al.*, (1994) *J. Biol. Chem.* 269, 15223-15228). As shown in Figures 16 and 18, inclusion of wild-type PAI-1 promoted greater endocytosis and degradation of ^{125}I-thrombin compared to mutant PAI-1. In contrast, the endocytosis of ^{125}I-uPA was enhanced to the same degree by either wild-type or mutant PAI-1 (Figures 17 and 19). RAP treatment blocked the wild-type PAI-1-promoted endocytosis of both thrombin and uPA. The results indicated that PAI-1 binding to Vn derived from serum is important for the clearance of thrombin. The present inventors believe that the clearance of free thrombin requires complex formation with PAI-1, a process known to be greatly accelerated by Vn. The low level of thrombin clearance promoted by mutant PAI-1 was likely due its ability to form a complex with thrombin, albeit inefficiently, in the absence of Vn. Given that heparin also stimulates complex formation although less efficiently than Vn (Gebbink, R.K. *et al.*, (1993) *Biochemistry* 32, 1675-1680), proteoglycans present in the cell culture may act to accelerate complex formation in lieu of Vn. Since PAI-1 binds uPA with high affinity without a requirement for Vn, uPA clearance (Figures 17 and 19) was not expected to depend on the ability of PAI-1 to complex with Vn.

To show that the PAI-1 mutation did not effect the ability of its complex with thrombin to bind to LRPs, complexes of ^{125}I-thrombin with either wild-type PAI-1 or mutant PAI-1 were formed *in vitro*. As shown in Figures 20-21, both types of complexes were readily endocytosed (Fig. 20) and degraded (Fig. 21) by the pre-type II pneumocytes. Both endocytosis and degradation were inhibited by RAP.

These results indicate that complexes of thrombin and either wild-type or mutant PAI-1 are recognized equally by LRP receptors. Therefore, when free ^{125}I-thrombin was presented to cells as in Figures 16-19, the complex formation with PAI-1:Vn was required for efficient complex formation between thrombin and PAI-1 which led to rapid LRP-mediated endocytosis and degradation.

PAI-1-promoted endocytosis and degradation of thrombin is augmented by <u>native but not conformationally-altered Vn</u>

It is known that native Vn accelerates the formation of the thrombin:PAI-1 complex whereas conformationally altered Vn does not (Naski *et al.*, *supra*). To determine whether the conformational state of Vn influenced PAI-1-mediated cellular clearance of thrombin, studies examined the clearance of ^{125}I-thrombin in the presence of PAI-1 and either native or conformationally altered Vn. As shown in Figures 22 and 24) (using cells grown in the absence of serum to eliminate exposure to serum Vn), exogenous native Vn enhanced ^{125}I-thrombin clearance. Conformationally altered Vn was no more effective in promoting the clearance of ^{125}I-thrombin than was PAI-1 alone. Given that glycosaminoglycans have been shown to promote inhibition of thrombin by PAI-1, proteoglycans may have contributed the low level of thrombin clearance observed with PAI-1 alone or PAI-1 plus conformationally altered Vn. By comparison, ^{125}I-uPA clearance mediated by complexing with PAI-1 was not influenced by native or conformationally altered Vn (Figures 23 and 25).

III. Discussion

Based on these findings, it was concluded that active thrombin clearance by pre-type II pneumocytes is mediated through complex formation with PAI-1 and the subsequent interaction of the complex with either LRP-1 or LRP-2. The role of native Vn in this process is critical, presumably due to the fact that it augments the formation of the thrombin:PAI-1 complex which is otherwise inefficient.

Vn binds both PAI-1 and thrombin. These binding interactions apparently lead to more efficient interaction between PAI-1 and thrombin. It is not known whether Vn remains associated with PAI-1 and thrombin following their interaction. Vn forms a ternary complex with thrombin bound to either ATIII, HCII, proteinase nexin I or α_1AT-Pittsburgh (Ill, C. R. *et al.* (1985) *J. Biol. Chem.* *260*, 15610-15615; Rovelli, G. *et al.*, (1990) *Eur. J. Biochem. 192*, 797-803; Tomasini, B.R. *et al.* (1989) *Biochemistry 28*, 7617-7623). However, the PAI-1:Vn complex dissociates following the interaction with either uPA or tPA. The above experiments did not evaluate whether Vn was endocytosed along with thrombin:PAI-1 complex. Other studies showed that active thrombin but not inactivated thrombin promoted the cellular clearance of ^{125}I-native Vn. (Panetti, T.S. *et al.* (1993) *J. Biol. Chem. 268*, 11988-11993). Since inactive thrombin

does not bind serpins whereas active thrombin can, the authors speculated that an interaction between thrombin and some endogenous inhibitor facilitated native Vn clearance. This is consistent with the present findings of (a) active thrombin being cleared more efficiently than inactivated thrombin and (b) PAI-1 antibodies inhibiting the clearance of active thrombin. The results indicate the possibility that a ternary complex of thrombin:PAI-1 and Vn may be cleared. The fact that RAP blocks thrombin clearance to the same extent as excess unlabeled thrombin indicates that LRP receptors are primarily responsible for mediating the clearance process.

A major concept to emerge from this study is that PAI-1 mediates thrombin catabolism but it raises the question of when and where this might occur *in vivo*. While PAI-1 inhibits uPA and tPA with a second-order rate constants of 10^7 $M^{-1}sec^{-1}$, the second-order rate constant for inhibition of thrombin is about 10,000-fold less. The physiological relevance of PAI-1 inhibition of thrombin may not be immediately obvious until one considers that cofactors such as heparin and Vn dramatically enhance the ability of PAI-1 to inhibit thrombin. For example, in the presence of Vn the second-order rate constant for the inhibition of thrombin by PAI-1 is increased by more than two orders of magnitude. This effect makes PAI-1:Vn a 10-20-fold better inhibitor of thrombin than ATIII (in the absence of heparin). However, in blood, where the concentration of ATIII is 10,000-fold higher than PAI-1, PAI-1 as not likely to be an important inhibitor of circulating thrombin. In extravascular sites such as in the recesses of a fibrin-containing thrombus, the present inventors believe that PAI-1 may act as a physiological inhibitor of thrombin. Fibrin is thought to sequester thrombin, protecting it from circulating inhibitors until lysis of the clot by plasmin. The thrombin thereby released would be available to drive post-clotting events such as mitogenesis and chemotaxis of cells involved in clot remodeling and tissue repair. PAI-1, derived from (a) platelets or (b) synthesized by cells invading a clot or on the boundaries of the clot, and Vn derived from either platelets or blood, could inactivate thrombin and promote its clearance by LRP-expressing cells (*e.g.* smooth muscle cells, macrophages, fibroblasts). This could be the mechanism for the negative regulation of the post-clotting effects of thrombin.

EXAMPLE III

Interaction of Different Conformers of PAI-1 with Vitronectin (Vn)

The inventors examined the binding of 6 different conformational forms of PAI-1 to both native and urea-treated Vn. The results indicate that only the active form of PAI-1 binds to Vn with high affinity and suggest that the Vn-binding domain of PAI-1 is sensitive to the conformation of PAI-1 and thus its activity state. The findings suggest that the binding epitope on PAI-1 may have evolved such sensitivity to prevent the accumulation of inactive PAI-1 at sites of subcellular attachment.

Materials

Purified PAI-1 either, active (>95%) or latent (>95%) were obtained from Molecular Innovations (Royal Oak, MI). The PAI-1 mutant Q123K has been previously described, and was purified to homogeneity in either the active or latent conformation as described (Kounnas, M.Z., *et al.*, (1992) *J. Biol. Chem.* 267:12420-12423). Purified Vn, both native (Naski, M. C. *et al.*, (1993) *supra*) ("nVn") and urea-purified ("dVn") were obtained from Drs. D. Mosher and T. Podor, respectively. Recombinant high molecular weight uPA was obtained form Dr. J. Henkin of Abbott Laboratories, and tPA (Activase) was from Genentech. Porcine pancreatic elastase was from Elastin Products, and bovine β-trypsin and β-anhydrotrypsin were prepared as by conventional means. The eight residue synthetic peptide Ac-Thr-Val-Ala-Ser-Ser-Ser-Thr-Ala corresponding to the PAI-1 reactive center loop from P_{14} to P_7, residues 333-340 of SEQ ID NO:3, was synthesized by the University of Michigan Biomedical Research Core Facilities.

Generation of cleaved and complexed forms of PAI-1

PAI-1 cleaved at the P4 position of the reactive center loop (Lawrence, D. A., *et al.*, (1994) *J. Biol. Chem.* 269:27657-27662) was produced by treatment of 4.6μM active PAI-1 with a 1/10 molar equivalent of elastase for 30 min. at 23°C in Tris buffered saline, pH 7.5 (TBS) followed by treatment of the sample with 1 mM (final concentration) of PMSF to inactive the elastase. PAI-1 complexes with uPA and tPA were formed by incubation of 1.5 molar equivalents of either enzyme with 4.6μM active PAI-1 for 30 min. at 23°C in TBS, followed by inactivation of

residual enzyme by 1mM (final concentration) of APMSF. Following incubation with either PMSF or APMSF all samples had no detectable enzymatic activity, and SDS-PAGE analysis indicated only trace amounts of unreacted PAI-1 in each sample. This residual unreacted PAI-1 is believed to represent the small amount of latent PAI-1 contained in the active PAI-1 preparation. Complexes with bovine β-trypsin were formed by reacting 26 μM active PAI-1 with 13 μM trypsin in 25 mM sodium phosphate, 125 mM NaCl, 0.5 mM EDTA, 10 mM $CaCl_2$, pH 6.6 for 30 min. at 23°C, after which the remaining active PAI-1 was removed by chromatography on uPA-agarose. SDS-PAGE analysis indicated that the complexes contained no detectable uncleaved PAI-1 and about 20 % free cleaved PAI-1. The PAI-1-peptide complex was produced by incubating 6.4μM active PAI-1 with 200μM peptide in 0.1M HEPES, 0.1 M NaCl, 1 % PEG-8000, 0.1% Tween-80, pH 7.4 at 25°C until no detectable PAI-1 inhibitory activity remained. The free peptide was then removed by chromatography on Heparin Sepharose. PAI-1-peptide complex formation was confirmed by thermodenaturation, mass spectra analysis, and by SDS-PAGE with and without tPA. The latter analysis indicated that the peptide annealed PAI-1 was a substrate for tPA and contained approximately 15% latent PAI-1, consistent with previous studies.

Assay for various PAI-1 conformational forms binding to Vn:

PAI-1 binding to immobilized Vn was determined as previously described ((Lawrence, DA, *et al.* (1994) *J Biol. Chem. 269*, 15223-15228)). Briefly, Vn at 1μg/ml in phosphate buffered saline (PBS), was coated overnight onto Immulon 2 (Dynatech) microtiter plates in a volume of 100μl at 4°C, and all subsequent steps were performed at room temperature. The plates were washed with PBS followed by dH_2O, allowed to air dry for 15 min., and then blocked with 200μl of 3% bovine serum albumin in PBS for 30 minutes. Next, PAI-1 containing samples were added, in a final volume of 100μl, and incubation continued for one hour. Bound PAI-1 was then detected with affinity purified, biotinylated, rabbit anti-PAI-1 antibodies (Sherman, P. M., *et al.* (1992) *J. Biol. Chem. 267*:7588-7595) and streptavidin conjugated to alkaline phosphatase using the substrate p-nitrophenyl phosphate, disodium (Sigma) at a concentration of 4mg/ml in 100mM Tris-HCl pH.9.5, 5 mM $MgCl_2$. For analysis of the PAI-1-anhydrotrypsin complex binding

to Vn, 1 μM (final concentration) of anhydrotrypsin was included in all wells during the PAI-1 incubation step. This concentration of anhydrotrypsin was 20-fold higher than the highest concentration of PAI-1 tested, and ten-fold higher that the reported K_d for the interaction of PAI-1 and anhydrotrypsin.

RESULTS

Figure 26 demonstrates that pure active PAI-1 binds to both forms of Vn with high affinity. However, the K_d for dVn is nearly 10-fold lower than for nVn (150pM compared to 1.4nM). In contrast pure latent PAI-1 binds to both forms of Vn with much lower affinity (K_d >225nM). These results support the contention that only active PAI-1 binds to Vn with high affinity and contradict the suggestion that both forms of PAI-1 bind to Vn with equal affinity. The relative K_d 's calculated form the data in Figure 14 are also consistent with previously reported values. Thus, the reported K_d of 50-190nM is much closer to the present estimate. (The K_d values must be estimates since the binding did not saturate at the concentrations tested.] For latent PAI-1 binding to either native Vn or dVn, the K_d > 225nM (Fig. 26).

The observation that latent PAI-1 binds to Vn with a much lower affinity than active PAI-1 suggests that the conformational change associated with conversion to the latent form may be responsible for the reduced affinity. The present inventors and their colleagues (Lawrence *et al., 1994*, supra) had suggested that stabilization of PAI-1 by Vn occurs when Vn binding to strand 1 of β-sheet A limits the mobility of β-sheet A necessary for insertion of the PAI-1 RCL during transformation to the latent conformation. This model is consistent with the observation that reconstitution of the serpin β-sheet A from a five stranded primarily parallel β-sheet into a six stranded antiparallel β-sheet by insertion of the RCL into β-sheet A as strand 4, requires extensive rearrangement of β-strands 1, 2 and 3 of sheet A (Stein, P. *et al.*, (1991) *Mol. Biol. 221*:615-621). Restriction of this rearrangement by Vn could retard loop insertion and thus the conversion of PAI-1 to the latent form. The inventors predicted that rearrangement of sheet A would also modify the Vn binding pitope on PAI-1. This proposal was supported by the results shown in Figure 14 indicating that

latent PAI-1, which has a reorganized β-sheet A, binds both forms of Vn with a markedly reduced affinity compared to active PAI-1.

The present inventors and colleagues investigated the binding of four additional forms of PAI-1 to both native and dVn, and like latent PAI-1, each of these conformers is thought to have its β-sheet A in the six stranded form. They include:

(1) PAI-1 in a stable complex with either uPA or tPA, which was previously shown to be cleaved at the P_1 position of the RCL and to have the RCL inserted into β-sheet A;

(2) Cleaved PAI-1 that is uncomplexed but has a reconstituted β-sheet A; and

(3) PAI-1 annealed to a synthetic RCL peptide, which has an intact RCL that is not inserted into β-sheet A, but has a reconstituted sheet A due to insertion of the synthetic peptide to form strand 4 of sheet A (Kvassman, J. *et al*, (1995) *J Biol. Chem. 270*:27942-27947).

The results are shown in Figure 15, and demonstrate that, like latent PAI-1, none of the other PAI-1 conformers bound to nVn with high affinity (estimated relative K_ds >100 nM). Similar results were obtained with dVn.

The relatively low affinity observed for both the tPA-PAI-1 and uPA-PAI-1 complexes with both forms of Vn is consistent with previous reports that tPA can dissociate PAI-1 from soluble Vn (Declerck *et al.*, 1988, *supra*), and that PAI-1 can be removed from ECM by treatment with uPA (Mimuro *et al.*, 1987, *supra*). Interestingly, PAI-1 in complex with the synthetic RCL peptide shows the same reduced affinity for Vn as the other conformers. This indicates that cleavage of the RCL is not required for the loss of binding affinity, but that it is the reorganization of β-sheet A that is necessary, since in the PAI-1-peptide complex the natural RCL remains intact (Kvassman, 1995, *supra*). Taken together, the results suggest that the Vn-binding epitope of PAI-1, which includes strand 1 of β-sheet A, is sensitive to conformational changes in β-sheet A.

To confirm that it is the rearrangement of sheet A that is responsible for the loss of affinity and not simply the association of PAI-1 with an enzyme, the relative binding affinity of PAI-1 in complex with either trypsin or anhydrotrypsin was tested. PAI-1 is an efficient inhibitor of trypsin and forms SDS-stable, RCL

inserted complexes just as with uPA or tPA. In contrast, anhydrotrypsin binds to the PAI-1 RCL in a non-covalent association that does not result in cleavage of the RCL or its insertion into β-sheet A. These results are shown in Fig. 28 and indicate that like uPA and tPA, PAI-1-trypsin complexes have a very low affinity for Vn. However, PAI-1 in association with anhydrotrypsin binds to Vn with essentially the same affinity as active PAI-1 alone. This indicates that it is not the binding of an enzyme to the RCL that results in loss of Vn affinity but that it is cleavage of the RCL and subsequent insertion of the loop into β-sheet A. The results strongly suggest that the reorganization of β-sheet A leads to the reduction in PAI-1's affinity for Vn.

Presently, there has been only one region on PAI-1 that has been shown to interact with Vn (Lawrence *et al.* 1994, *supra*; Van Meijer *et al.* (1994) *FEBS Lett.* *352*:342-346; Padmanabhan, J. *et al.* (1995) *Thromb. Haemost* *73*:829-834), and our data suggest that this site loses affinity for Vn following rearrangement of β-sheet A. However, PAI-1 may have two independent binding sites for Vn, one with high affinity that is only expressed on active PAI-1 and one with low affinity that is present on all conformations. While it is impossible to completely distinguish between these two possibilities, if the latter were true, then mutations that affect one site would not necessarily affect the other site. Conversely, if the different forms of PAI-1 interact with Vn through the same, though conformationally altered, site then a single point mutation in PAI-1 could affect binding in both high and low affinity interactions. Accordingly, the PAI-1 point mutation Q123K that has a greatly reduced affinity for Vn was purified and the active and latent forms separated and examined for Vn binding (Fig. 29). Comparison of the binding of active and latent Q123K PAI-1 to nVn with the binding of active and latent wtPAI-1 indicated that both the active and latent forms of the mutant bind to nVn with lower affinity relative to their wtPAI-1 counterpart. Similar results were obtained when dVn was used. This suggested that both the high and low affinity interactions utilize the same or at least overlapping binding epitope(s) on PAI-1, since they are affected to a similar extent by the Q123K mutation. This mutation has no affect on the inhibitory activity of PAI-1 or on its affinity for heparin-Sepharose, indicating that the affects of the mutation are local.

and do not introduce significant global changes in the PAI-1 structure. Comparing the surface accessibility of Q123 on a model of active PAI-1 to its accessibility in the latent structure indicate that in latent PAI-1 Q123 becomes partially obscured by surrounding residues compared to its exposure in the active form. This is consistent with the loss of affinity for Vn observed with latent PAI-1, and support the notion that PAI-1 contains only one binding epitope for Vn which is conformationally sensitive.

Recent studies of the serpin mechanism of inhibition indicate that it follows a multi-step process that requires an exposed RCL (Shore *et al.* 1994, *supra*, Lawrence *et al.*, 1995, *supra*; Fa, M. *et al.* (1995) *Biochem.* *34*:13833-13840; Wilczynska, M. *et al.* (1995) *J. Biol. Chem.* *270*:29652-29655). Upon association with a target proteinase the serpin RCL is cleaved at its P1-P1' bond and this is followed by a rapid insertion of the RCL into β-sheet A yielding the stable serpin-proteinase complex. In the present study we demonstrate that the PAI-1 Vn binding epitope on the edge of β-sheet A is sensitive to this conformational change in β-sheet A, as well as to similar changes associated with conversion of PAI-1 to the latent form or cleavage in the RCL by a non-target proteinase. This sensitivity may provide a way to ensure the expression of PAI-1 activity at specific sites of action. For example, it is thought that Vn serves to localize PAI-1 to the ECM where it regulates local proteolytic activity (Mimuro *et al.*, 1987, *supra*). In this situation it may be beneficial to permit only functionally active PAI-1 to bind to Vn. On a cell surface, an inactive ligand can be internalized and degraded. However, this type of regulation may not be as efficient on the less dynamic ECM. Therefore, to prevent Vn from becoming saturated with inactive forms of the inhibitor, a system may have evolved that is sensitive to the conformation of PAI-1 which is closely linked to its activity state.

EXAMPLE IV

PAI-1 Prevents Integrin Vitronectin Receptor ($\alpha_v\beta_3$)-Mediated Cell Migration by Blocking the RGD Cell Attachment Site on Vitronectin

The PAI-1 binding site on Vn was recently localized to the first 50 amino acid residues. This region also contains the RGD (Arg-Gly-Asp) cell attachment site. To determine whether these binding sites overlap, competition studies

between purified VnR and PAI-1 were performed. The competition of active wtPAI-1 was compared to two different PAI-1 mutants. One, Q123K-PAI-1 has a single amino acid substitution, that does not affect inhibitory activity, but reduces its affinity for Vn approximately 2 orders of magnitude. The second, P1Ala-PAI-1 also has a single substitution (R346A) that destroys its ability to inhibit PAs, but has no affect on Vn binding.

Materials and Methods

Active forms of wtPAI-1 and the PAI mutants were prepared as described (Kvassman, J. *et al.*, *Fibrinolysis* 9:120-125 (1995)). Native Vn (Molecular Innovations) was coated to microtiter wells (1μg/ml) for 2 hours at 37°C, followed by blocking with 2%BSA in 50mM Tris, pH 7.5 containing 100mM NaCl and 5mM $CaCl_2$ (Binding buffer). Vitronectin receptor (VnR) ($\alpha_v\beta_3$ integrin) was purified from human placenta as described (Smith, J.W. *et al.*, *J. Biol. Chem.* *265*:11008-11013 (1990)). Radiolabeled VnR (2.5nM) was allowed to bind to microtiter wells in the presence of increasing concentrations of either wild-type PAI-1, Q123K-PAI-1 or P1Ala-PAI-1. The samples were processed as described (Stefansson, *et al.*, 1995, *supra*). The results (shown in Fig. 30) were plotted using the program "Grafit" and represents three experiments performed in duplicate.

In the experiment shown in Figures 31 and 32, ^{125}I-VnR (5nM) was allowed to bind to native Vn (Fig. 31) or fibronectin (Fig. 32) coated on microtiter plates in the presence of wtPAI-1 (500nM), and P1-Ala-PAI-1 (500nM), unbound PAI-1 was removed and uPA (400nM) was added where indicated. A mAb specific for integrin $\alpha_v\beta_3$, LM609 (50μg/ml), was incubated similarly as a positive control for inhibition of binding. Samples were incubated and developed as described above (for Fig. 30). The results represents 2 experiments, each performed in duplicate.

In the study depicted in Figures 33-34, rabbit SMC were detached using a non-enzymatic cell dissociation solution (Sigma). Cells were resuspended in serum-free medium containing either wtPAI-1, Q123K-PAI-1 or P1Ala-PAI-1 (75nM final concentration) and allowed to attach for 30 min at 37°C. The plates were washed and stained using 2% crystal violet. Cells were counted on two

random fields in duplicate wells. The results represent 4 experiments performed in duplicate.

In the next study, Transwells were coated with Vn and blocked as described above for Fig. 30. Rabbit SMC were detached using a mild trypsin treatment, washed in 0.5mg/ml trypsin inhibitor and pelleted by centrifugation. Cells were allowed to attach and spread on the upper chamber in serum-free medium (0.5-1 hour) before PAI-1 (500nM) was added. After 30 min incubation, serum was added, and the wells were incubated for 3-4 hours. Migrated cells were stained and counted.

Results

Both active wtPAI-1 and P1Ala-PAI-1 were found to be efficient competitors of the binding of purified ^{125}I-VnR to native Vn (K_i was about 4nM, Fig. 30). In contrast, Q123K-PAI-1 was a poor competitor of VnR binding, yielding an estimated K_i greater than 100 nM. Together, these results demonstrated that the high affinity of PAI-1 for Vn, and not the ability of PAI-1 to inhibit PAs, is responsible for the inhibition of VnR binding to Vn.

Neither the wt PAI-1 nor the two different PAI-1 mutants affected binding of ^{125}I-VnR to fibronectin, indicating the specificity of the interaction for Vn.

PAI-1 undergoes profound conformational changes upon inhibition of a proteinase (Shore *et al.*, 1995, *supra*), which leads to loss of its high affinity for Vn. Therefore, PAs might be expected to regulate the ability of PAI-1 to block the RGD site on Vn. To examine this possibility, competition assays were performed with and without uPA. uPA in 2-fold molar completely blocked the inhibition of ^{125}I-VnR binding to Vn by wtPAI-1 (Figures 31-32). These findings are in accord with the observation that the PAI-1:uPA complex has significantly lower affinity for Vn than does the VnR, allowing the VnR to displace the PAI-1:uPA complex. As expected, P1Ala-PAI-1 did not reduce the inhibition of VnR binding in the presence of uPA, consistent with the mutant's lack of reactivity with uPA.

A mAb specific for integrin $\alpha_V\beta_3$, LM609, inhibited the binding of ^{125}I-VnR to Vn to the same extent as did PAI-1, indicating that (a) the VnR preparation contained primarily $\alpha_V\beta_3$ and (b) PAI-1 specifically blocked the binding of $\alpha_V\beta_3$ to Vn (Figures 31-32).

To test whether PAI-1 could similarly inhibit the interactions of cells with Vn, adhesion and migration assays were performed with vascular smooth muscle cells (SMC). Both active wtPAI-1 and P1Ala-PAI-1 inhibited adhesion of SMC to Vn (Figures 33-34). In contrast, Q123K-PAI-1 did not inhibit adhesion, indicating that the binding of PAI-1 to Vn, and not the ability of PAI-1 to inhibit PAs, was responsible for blocking cell attachment. Furthermore, addition of uPA to wtPAI-1 bound to Vn prevented the inhibition of cell attachment whereas uPA had no affect on the inhibition of SMC attachment by P1 Ala-PAI-1.

Interestingly, whereas PAI-1 inhibited adhesion of SMC, the mAb to $\alpha_V\beta_3$ did not, indicating that SMC must have other integrins that play a role in attachment to Vn, and that PAI-1 blocks access to all of these adhesion molecules. Consistent with the results using purified VnR, PAI-1 had no effect of SMC adhesion to fibronectin.

Active wtPAI-1 and R346A-PAI-1 also inhibited SMC migration, as measured in Transwells coated with Vn. This inhibition was similar to that caused by LM609. The Q123K-PAI-1 mutant did not inhibit migration. As with cell attachment, inclusion of uPA reversed the inhibition by wtPAI-1 but not by P1Ala-PAI-1.

Wound conditions were simulated *in vitro* using a razor cut monolayer model. Migration and adhesive properties of type II pneumocytes on a Vn-coated surface were observed microscopically. The results indicated that the PAI-1 mutant with low affinity for Vn had no effect on cell migration. Wild type PAI-1 inhibited migration. The presence of P1 Ala PAI-1 mutant not only prevented migration but actually resulted in holes in the monolayer itself indicating detachment of cells from the plate. The anti-Vn antibody had similar effects. In contrast, wild type PAI-1, which binds normally to the Vn binding site, had an intermediate effect above with thinning of the monolayer due to inhibition of migration, but without the stark effect of the holes which were caused by the P1 Ala mutant.

Discussion

Vn has known profound effects on the properties of PAI-1. In addition to stabilizing PAI-1 in the active conformation (Declerck, P. *Verh. K. Acad.*

Geneeskd. Belg. 55:457-473 (1993)). Vn also alters the specificity of PAI-1, rendering it an efficient inhibitor of thrombin (Naski *et al.*, *supra*) and mediating the clearance of thrombin by cellular receptors (see above). Based on this, the present inventors conclude that thrombin, a known mitogen and chemoattractant (Bar-Shavit, R. *et al.*, *Cell Regul. 1*:453-463 (1990)) may promote cell migration by removing PAI-1 from Vn. Others have shown that both elastase and cathepsin G produced by activated neutrophils can efficiently remove PAI-1 from the matrix (Wu, K. *et al.*, *Blood 86*:1056-1061 (1995)). Since PAI-1 is a substrate for these latter proteinases, only catalytic amounts would be required to inactivate PAI-1. This could account in part for the remarkable ability of these cells to migrate.

Together, the above findings indicate that a wide variety of proteinases, even those which are not targets for PAI-1, are able to interact with PAI-1 and expose the RGD integrin binding site on Vn. Such a general ability of many divergent proteinases to modify cellular adhesive properties through a common mechanism suggests that the known relationship between increased cell migration and proteinase activity in a wide variety invasive cellular processes is mediated at least in part by proteolytic interaction with PAI-1. The present inventors also conclude that the role of proteinases in cellular migration may not simply be that of generalized matrix degradation but rather the generation of cell attachment sites through specific interaction with PAI-1.

EXAMPLE V

Characterization of the Binding of Different Conformational Forms of PAI-1 to Vitronectin

The inventors examined the binding of different conformational forms of PAI-1 to both native Vn (nVn) and urea-purified Vn (uVn) using a solid phase binding assay and found that active PAI-1 binds to uVn with approximately 6-fold higher affinity than to nVn. In contrast, inactive forms of PAI-1 (latent, elastase cleaved, synthetic reactive center loop peptide annealed, or complexed to PA's) displayed greatly reduced affinities for both forms of adsorbed Vn, with relative affinities reduced by more than 2 orders of magnitude. Structurally, these inactive conformations all differ from active PAI-1 by insertion of an additional strand into β-sheet A, suggesting that the rearrangement of sheet A is responsible for reduced Vn affinity. This is further supported by the observation that PAI-1 associated with b-anhydrotrypsin (which does not undergo rearrangement of β-sheet A) showed no decrease in affinity, whereas PAI-1 complexed to b-trypsin (which does undergo sheet A rearrangement) displayed reduced affinity for Vn similar to PAI-1:PA complexes. Together the results demonstrate that the interaction between PAI-1 and Vn depends on the conformational state of both proteins, and suggest that the Vn binding site on PAI-1 is sensitive to structural changes associated with loss of inhibitory activity.

As described above, PAI-1 bound to Vn in the extracellular matrix has been shown to block the binding of integrins (Stefansson, S. *et al.* (1996) *Nature 383*:441-443) and uPAR (Deng, G. *et al.* (1996) *J. Cell Biol. 134*:1563-1573) to Vn , and this interaction inhibited cell adhesion and migration on Vn. The precise nature of the PAI-1/Vn interaction has been the subject of considerable debate. Using solid-phase binding assays to quantitate this interaction, several studies mentioned above suggested that only active PAI-1 binds Vn; however, others reported no apparent difference in the binding of active and latent PAI-1 (Salonen *et al. supra*;, Kost *et al.*, *supra*). In addition, the reported dissociation constant for PAI-1 binding to immobilized Vn ranges from 0.3 nM to 190 nM. The Vn binding domain within PAI-1 is localized to a region on the surface of PAI-1 that includes b-strand 1A. The Vn binding site for PAI-1 appears to be localized to the

somatomedin B domain at the N-terminus of Vn, although other reports suggested that PAI-1 binds to the C-terminus of Vn between residues 348 and 370 (Kost *et al.*, *supra*), or to a site near the center of Vn between amino acids 115 and 121 (Mimuro *et al.*, *Biochemistry* 32:2314-2320 (1993)).

The present inventors postulated that a critical dependence of the PAI-1/Vn interaction on the PAI-1 and/or Vn conformation could explain these conflicting reports. To test this hypothesis the following studies were performed in which the binding of PAI-1 in six different conformations to immobilized nVn and uVn were examined. The results indicated that the two forms of Vn bind to PAI-1 with markedly different affinities and that the Vn binding domain on PAI-1 is very sensitive to the PAI-1 conformation. There may have been an evolutionary selection of the PAI-1 structure to permit efficient removal of inactive PAI-1 at sites of subcellular attachment.

Experimental Procedures

Materials. Purified PAI-1, either active (> 95%) or latent (> 95%), were obtained from Molecular Innovations (Royal Oak, MI). To eliminate any active PAI-1 present in the latent preparations, latent PAI-1 was treated with a 1/100 molar equivalent of elastase for 30 min. at 23°C in Tris buffered saline, pH 7.5 (TBS) followed by inactivation of the elastase with 1 mM (final concentration) PMSF. Purified nVn was obtained from Dr. D. Mosher, and uVn was either received from Dr. T. Podor or purchased from Calbiochem. Recombinant high molecular weight uPA was obtained from Dr. J. Henkin of Abbott Laboratories, and tPA (Activase) was from Genentech. Porcine pancreatic elastase was from Elastin Products, and bovine b-trypsin and b-anhydrotrypsin as described earlier The eight residue synthetic peptide Ac-Thr-Val-Ala-Ser-Ser-Ser-Thr-Ala corresponding to the PAI-1 reactive center loop from P_{14} to P_7, residues 333-340, was synthesized by the University of Michigan Biomedical Research Core Facilities.

Generation of cleaved and complexed forms of PAI-1 was accomplished as described in Example III, *supra*.

PAI-1 binding to Vn was determined either functionally as describe din Example III, or in a Vn specific ELISA as previously described (Lawrence *et al.*,

1994, *supra*. Briefly, Vn at 1 µg/ml in phosphate buffered saline (PBS), was coated overnight onto Immulon 2 (Dynatech) microtiter plates in a volume of 100 µl at 4°C, and all subsequent steps were performed at room temperature. The plates were washed with PBS followed by dH_2O, allowed to air dry for 15 min., and then blocked with 200 µl of 3% bovine serum albumin in PBS for 30 minutes. Next, PAI-1 samples in TBS, containing 100 µg/ml BSA and 0.01% Tween 80 were added, in a final volume of 100 µl, and incubation continued for one hour, after which the unbound PAI-1 was washed away. During this incubation period < 15 % of the active PAI-1 should have converted to the latent form, since we have determined the $t_{½}$ for this conversion to be ~ 8 hours at 25° C in the absence of Vn (data not shown). In the functional assay PAI-1 binding was determined by reacting the bound PAI-1 with 0.7 nM uPA for 30 minutes followed by the addition of the chromogenic substrate S-2444 (Kabi) as described by Lawrence *et al.*(*J. Biol. Chem. 265* :20293-20301 (1990)). The PAI-1 bound was then calculated from the loss of uPA amidolytic activity. K_ds for the solid-phase binding of PAI-1 to immobilized Vn were calculated using the following form of the standard binding equation from the GraFit program (Erithacus Software):

Equation 1: $y = [L]Cap / (K_d + [L])$

where y is the amount of PAI-1 bound, L is free PAI-1 and "Cap" is the Vn capacity for PAI-1 binding.

The Vn dependent ELISA assay was performed as above except that bound PAI-1 was detected with affinity purified, biotinylated, rabbit anti-PAI-1 antibodies and streptavidin conjugated to alkaline phosphatase using the substrate p-nitrophenyl phosphate, disodium (Sigma) at a concentration of 4 mg/ml in 100 mM Tris-HCl pH 9.5, 5 mM $MgCl_2$. To control for nonspecific binding all assays were simultaneously analyzed on plates coated with BSA alone and processed in parallel. The background binding to BSA was subtracted from all samples prior to data analysis. For examination of the PAI-1-anhydrotrypsin complex binding to Vn, 1 µM (final concentration) of anhydrotrypsin was included in all wells during the PAI-1 incubation step. This concentration of anhydrotrypsin was 20-fold higher than the highest concentration of PAI-1 tested, and ten-fold higher than the

reported K_d for the interaction of PAI-1 and anhydrotrypsin (17). For data analysis of ELISA experiments, the K_d was estimated for active PAI-1 with equation 1 above by assuming that PAI-1 bound as a percent of the maximal binding was proportional to the actual PAI-1 bound and that free PAI-1 was approximately equal to PAI-1 added. For the inactive PAI-1 samples examined no value for K_d could be established since none of these samples achieved saturation at the concentrations tested.

<u>Competitive inhibition of PAI-1 binding to immobilized Vn by solution-phase Vn</u>

Microtiter plates were coated with nVn, and blocked with BSA as above. Next, either native or urea-purified Vn was added to the plate and serially diluted three-fold in TBS, containing 100 µg/ml BSA and 0.01% Tween 80, after which active PAI-1 was added to a final concentration of 2 nM (final volume 100 µl). The samples were allowed to react for 1 hour at 23°C, washed and bound PAI-1 determined as in the ELISA assay as above. IC_{50} values for the inhibition by solution-phase Vn were calculated using a four parameter logistic fit from the GraFit program (Erithacus Software). The K_d for solution-phase interactions of PAI-1 with Vn were determined by analysis of competition data by methods previously described (Olson, S.T. *et al.*, (1991) *Arch. Biochem. Biophys.* 286, 533-545). According to this analysis, the concentration of PAI-1 bound to the competitor Vn in solution is equal to the difference between the total PAI-1 concentration used in the presence of the competitor and the total PAI-1 concentration yielding an equivalent extent of saturation of the immobilized Vn in the absence of the competitor. The latter was calculated based on the fit of binding data in the absence of competitor Vn (Figure 37) by equation 1. Knowledge of the concentration of PAI-1 bound to competitor Vn in solution allowed calculation of the concentrations of free PAI-1 and free competitor Vn for the solution interaction from which K_d was calculated. Reasonable agreement was obtained for K_d values determined at competitor Vn concentrations yielding significant extents of displacement of PAI-1 from the immobilized Vn (>15%).

<u>Results and Discussion</u>

The basis for the debate in the literature concerning the interaction between Vn and PAI-1 may be the conformational variability of both proteins. This study directly examined the binding of alternative conformations of PAI-1 to both native and urea-purified Vn. Previously, we described a functional assay for PAI-1 binding to Vn, in which active PAI-1 was shown to bind specifically to surface adsorbed nVn in a dose dependent and saturable manner. This assay was used to compare the binding of active wtPAI-1 to both forms of immobilized Vn (Figure 35). These results demonstrated that both urea-purified and native Vn have a similar binding capacity for active PAI-1, and that active PAI-1 binds to both forms with high affinity. However, the calculated K_d for the immobilized uVn is approximately 6-fold lower than for immobilized nVn (127 ± 20 pM compared to 825 ± 190 pM). This difference may reflect the different conformational states of the two Vn preparations, since nVn is predominately monomeric, while uVn is a disulfide linked multimer. The observation that PAI-1 has a higher affinity for immobilized multimeric Vn than for immobilized monomeric Vn is consistent with the result that PAI-1 isolated from plasma is predominately complexed with a high molecular weight form of Vn even though the majority of Vn in plasma is monomeric.

Therefore, to see if solution-phase multimeric Vn also bound PAI-1 with higher affinity than solution-phase monomeric Vn, competitive inhibition assays were performed with both nVn and uVn competing for PAI-1 binding to immobilized nVn. These results shown in Figure 36 demonstrate that both uVn and nVn compete for PAI-1 binding to immobilized nVn. This suggests that PAI-1 binds to the same site on both nVn and uVn, either when the Vn is in solution or immobilized. Furthermore, solution-phase uVn is a more efficient competitor for PAI-1 binding (IC_{50}=65 nM) than is solution-phase nVn (IC_{50}=375 nM). This approximate 6-fold difference is similar to that shown in Figure 35, and indicates that either in solution or when immobilized, uVn has a higher affinity for PAI-1 than does nVn. K_d values of 20 ± 1.4 nM and 125 ± 12 nM for the interaction of PAI-1 with solution forms of uVn and nVn, respectively, were calculated from these data. This indicates that PAI-1 binds to immobilized Vn with a significantly higher affinity than to solution-phase Vn, having an approximately 150-fold higher

K_d for the solution-phase interaction with either form of Vn. This enhanced binding to immobilized Vn may result from the different conformation that Vn is known to assume when it adsorbs to a surface (Stockmann, A. *et al.*,. *J. Biol. Chem. 268*:22874-22882(1993); Preissner, K.T. *et al.*, *J. Biol. Chem. 265*:18490-18498 (1990)).

To examine the binding of alternative conformational forms of PAI-1, an ELISA based assay was performed similar to the solid-phase assay described above except that PAI-1 is detected with an anti-PAI-1 antibody, permitting analysis of inactive conformations of PAI-1. Figure 37 shows the binding of both active and latent PAI-1 to surface-adsorbed urea-purified and native Vn. Analysis of the binding of active PAI-1 to the two forms of immobilized Vn yields calculated K_ds of 150 ± 16 pM with uVn and 1300 ± 200 pM with nVn. These values are similar to those calculated using the PAI-1 functional assay (Figure 35), indicating that the indirect antibody assay is also suitable for evaluating PAI-1 binding to immobilized Vn. In contrast to active PAI-1, latent PAI-1 binds to both forms of immobilized Vn with much lower affinity. In this case a K_d could not be determined since saturable PAI-1 binding was not obtained at the concentrations tested. However, if we assume that latent PAI-1 is binding with the same stoichiometry as active PAI-1, then we can estimate a minimum value for K_d of > 225 nM (the highest concentration tested) in both cases (Figure 37). These results are consistent with previous reports that only active PAI-1 binds to Vn with high affinity, and contradict the suggestion by others that both forms of PAI-1 bind Vn with equal affinity .

The K_ds calculated for active PAI-1 binding to immobilized Vn were similar to previously reported values: 127 pM vs. 300 pM (Seiffert *et al.*, 1991, *supra*) with uVn, and 825 pM vs. 4.4 nM (Lawrence *et al.*, *J. Biol. Chem*, 1994, *supra*) with nVn. An earlier report that calculated a lower affinity K_d of 55-190 nM for these interactions using a similar assay failed to account for the presence of both active and latent PAI-1 in the preparation and may have been measuring primarily the binding of latent PAI-1 (Salonen *et al.*, *supra*). Consistent with this interpretation, the reported K_d of 190 nM is similar to our estimated minimum K_d for latent PAI-1 binding to either native or uVn (K_d > 225 nM) (Figure 37).

Salonen *et al.* also noted a high affinity, "low capacity" binding site (K_d < 100 pM) that may have represented the active PAI-1 in their preparation.

The observation that latent PAI-1 binds to Vn with a much lower affinity than active PAI-1 suggests that the conformational change associated with conversion to the latent form may be responsible for the reduced affinity. We suggested earlier (Lawrence *et al*, *supra*) that the stabilization of PAI-1 by Vn occurs when Vn binding to strand 1 of β-sheet A limits the mobility of β-sheet A necessary for insertion of the PAI-1 RCL during transformation to the latent conformation. This model is compatible with the observation that conversion of the serpin β-sheet A from a five stranded to a six stranded antiparallel β-sheet by insertion of the RCL as strand 4 of β-sheet A, requires extensive rearrangement of b-strands 1, 2 and 3. Restriction of this rearrangement by Vn could retard loop insertion and thus the conversion of PAI-1 to the latent form. Also consistent with this model is the apparent modification of the Vn binding site on PAI-1 following RCL insertion, as indicated by the reduced affinity of latent PAI-1 for Vn (Figure 37).

Next to be examined was the binding of native and uVn to PAI-1 complexed to tPA or uPA, cleaved by elastase, or inactivated by insertion of a synthetic RCL peptide. Each of these conformers is thought to have its β-sheet A in the six stranded form, similar to the structure of latent PAI-1. The results are shown in Figure 38. Like latent PAI-1, none of these RCL inserted forms of PAI-1 bound to immobilized nVn with high affinity, with all having estimated K_ds > 112-225 nM (the highest concentrations tested). Similar results were obtained with immobilized uVn. The relatively low affinity observed for both the tPA-PAI-1 and µPA-PAI-1 complexes with both forms of Vn is consistent with previous reports that tPA dissociates PAI-1 from solution-phase Vn, and that PAI-1 can be removed from extracellular matrix by treatment with uPA (Mimuro *et al.*, 1987, *supra*). Of note, PAI-1 in complex with the synthetic RCL peptide showed a reduced affinity for Vn similar to the other loop inserted forms. This indicates that it is not the loss of an exposed RCL that results in a reduction of binding affinity for Vn, since in the PAI-1-peptide complex the natural RCL remains intact and

fully accessible. Rather, it appears to be the reorganization of β-sheet A that leads to reduced affinity.

To confirm that rearrangement of sheet A (and not simply the association of PAI-1 with an enzyme) was responsible for the loss of affinity, the relative binding affinity of PAI-1 in complex with either trypsin or anhydrotrypsin was tested. PAI-1 is known to be an efficient inhibitor of trypsin and forms SDS-stable, RCL inserted complexes, as with uPA or tPA. In contrast, anhydrotrypsin binds to the PAI-1 RCL in a non-covalent association that does not result in cleavage of the RCL or its insertion into β-sheet A. Like uPA and tPA, PAI-1-trypsin complexes had a very low affinity for immobilized nVn (Figure 39). However, PAI-1 in association with anhydrotrypsin bound to immobilized nVn with nearly the same affinity as did active PAI-1 alone. This confirms that it is not simply the association of an enzyme with the RCL that leads to a loss of Vn affinity, but instead it is the enzyme induced insertion of the RCL into β-sheet A.

As discussed in other sections, above, recent studies indicate that the serpin mechanism of inhibition is a complex process requiring an exposed RCL. Upon association with a target proteinase the serpin RCL is cleaved at its P_1-$P_{1'}$ bond, and the RCL is inserted into β-sheet A, yielding the stable serpin-proteinase complex. Here, it has been demonstrated that the PAI-1 Vn binding site on the edge of β-sheet A was sensitive to this conformational change in β-sheet A, as well as to similar changes associated with conversion of PAI-1 to the latent form or cleavage in the RCL by a non-target proteinase. This sensitivity may provide a way to ensure the expression of PAI-1 activity at specific sites of action. For example, Vn is believed to localize PAI-1 to the extracellular matrix where it regulates local proteolytic activity (Mimuro *et al., supra*), and blocks cell adhesion and migration. In this setting it would be beneficial to permit only functionally active PAI-1 to bind to Vn. On a cell surface an inactive ligand can be internalized and degraded. However, this type of regulation may not be as efficient on the less dynamic extracellular matrix. It is proposed, therefore, that to prevent Vn from becoming saturated with inactive forms of PAI-1, a system sensitive to the conformational state of PAI-1, which in turn is closely linked to its activity state, has been selected during evolution.

EXAMPLE VI

The Serpin PAI-1 Inhibits Cell Migration by Blocking Integrin Binding to Vn

The following study shows that Vn significantly enhances SMC migration, and that the specific VNR is required for cell motility. Also demonstrated are (a) the overlap of the attachment site on Vn with the binding site for PAI-1 and (b) the blocking of SMC migration by the active conformation of PAI-1. This effect required high affinity binding to Vn and was not dependent on PAI-1's ability to inhibit PAs. Complex formation between PAI-1 and PAs resulted in loss of PAI-1 affinity for Vn and restored cell migration. These results provide a direct link between PAs and integrin-mediated cell migration, and show that PAI-1 can control cell-matrix interactions by regulating the accessibility of specific cell attachment sites. Hence, the localization of PA activity at sites of focal contact is apparently not there to initiate a proteolytic cascade leading to generalized matrix destruction, but rather is required to expose cryptic cell attachment sites necessary for SMC migration.

METHODS

A. PAI-1 Competition of ^{125}I-VNR binding to Vn

Active forms of wtPAI-1 (from Molecular Innovations) and PAI-1 mutants were prepared as described by Kvassman *et al.*, *supra*. Vn was coated onto plates as described in Example III. Radiolabeled VNR (2.5 nM) was allowed to bind Vn in the presence of increasing concentrations of wtPAI-1 or PAI-1 mutants. For analysis (with and without uPA), 500 nM PAI-1 was allowed to bind to Vn as above, unbound PAI-1 was then removed, and 5 nM ^{125}I-VNR added either alone or in the presence of 1mM uPA or 50 mg/ml LM609 (Chemicon). Assays were processed and analyzed as described.

B. Attachment and migration of rabbit SMC on Vn

(See Example IV for description of attachment methods.) Washed cells were resuspended in serum free media ± 500 nM of wtPAI-1, Q123K-PAI-1, or R346A-PAI-1 either alone, or with 1 mM uPA or with LM609 (5 µg/ml) alone.

Cells were allowed to attach to Vn coated plates (1 mg/ml) for 30 min., then washed twice with TBS, fixed in methanol/acetic acid (75/25 v/v), and stained with 2% crystal violet. Absorbance of stained cells was measured using a Sony CCD/RGB color video system with Image-1 software (Universal Imaging). Cell attachment to Vn alone was established as 100 %, and the attachment of each experimental condition was calculated as a ratio to this value. Analysis of known cell numbers treated similarly indicated that the absorbance was linear over the range of cells examined. Migration assays were performed on Transwells® (3 mm pore size) coated with Vn. SMC were allowed to attach and spread for 45 to 60 min. on the upper chamber in serum free media. Next, 0.5 μg/ml of LM609, or 1 μM wtPAI-1, or PAI-1 mutants with or without 2 mM uPA were added in 0.5% BSA, 1 mM $CaCl_2$, 0.5 mM $MnCl_2$ and Nutridoma® (Boeringer-Manheim). After 4-5 hours the upper cell layer was removed with a cotton swab and cells on the underside of the Transwell were fixed, stained and analyzed as above, with the amount of cell migration observed with Vn alone established as 100 %. Migration on Matrigel® with and without Vn was as above except that Transwells® were first coated with Matrigel® (1:20 dilution) in serum-free media overnight at 4°C, followed by washing with PBS and blocking with 1% BSA in PBS. Transwells were then incubated ± Vn (0.2 mg/ml) followed by washing with PBS prior to addition of cells. Migration was determined after 14-16 hours incubation.

RESULTS AND DISCUSSION

The interaction between cells and their substrata is an important regulator of cellular function. During wound healing, migrating cells exhibit enhanced expression of the Vn receptor (VNR) integrins, including which is transiently expressed at the leading edge of cells invading a fibrin clot (Vassalli, J.-D. *et al.*,(1991) *J. Clin. Invest. 88:*1067-1072). Like , urokinase plasminogen activator (uPA) is also located at the leading edge of migrating keratinocytes during the early stages of re-epithelization, and migrating vascular cells show elevated expression of uPA and its receptor (uPAR), which localize to focal contacts. Vn enhances this co-localization, and also accelerates the association of the VNR with vinculin at focal contacts. Thus, during wound healing, cells display a similar

pattern of expression for uPA and $\alpha_v\beta_3$ both temporally and spatially, suggesting a possible link between these two systems. *In vivo*, uPA and its inhibitor PAI-1 are important regulators of vascular wound healing. Mice deficient in uPA are protected from neointima formation following vascular injury. However, PAI-1 null mice exhibit excessive intimal thickening due to SMC migration and proliferation, and over-expression of PAI-1 reduces neointima formation to levels similar to uPA null mice. The traditional interpretation of these data is that PAs are required to initiate a proteolytic cascade at the cell-substratum interface that results in matrix destruction necessary for cellular migration and invasion (Declerck *et al.*, 1988, *supra*). However, in the current example provides results suggesting a more subtle role for PAs during wound healing, and demonstrating for the first time a direct link between PAs and the VNR integrins.

The PAI-1 binding site was recently localized to the first 50 residues of Vn, a region that also contains the RGD cell attachment site. To determine whether these binding sites overlap, competition studies between purified radiolabeled VNR and PAI-1 for binding to Vn were performed. Wild-type PAI-1 (wtPAI-1) efficiently competed with ^{125}I-VNR for binding to immobilized Vn (Figure 40). A mutant PAI-1 (R346A) that binds to Vn normally, but does not inhibit PAs, inhibited the binding of ^{125}I-VNR to Vn identically to wtPAI-1 (Ki ~ 4 nM). However, a second PAI-1 mutant (Q123K) that inhibits PAs normally, but has a significantly reduced affinity for Vn, was a relatively poor inhibitor of ^{125}I-VNR binding to Vn. These results demonstrate that PAI-1 binding to Vn was sufficient to block VNR binding. None of the PAI-1 variants had any effect on the binding of ^{125}I-VNR to fibronectin, indicating that the interaction is specific for Vn, and that the loss of VNR binding is not due to interactions between PAI-1 and the VNR.

PAI-1 undergoes profound conformational changes upon reaction with a proteinase. This structural change results in loss of high affinity for Vn and rapid clearance of the PAI-1:proteinase complex by members of the LDL receptor family. Therefore, to examine the possibility that PAs might regulate integrin attachment by decreasing the affinity of PAI-1 for Vn, competition assays were

performed in the presence and absence of uPA. In the presence of a 2-fold molar excess of uPA, the ability of wtPAI-1 to inhibit ^{125}I-VNR binding to Vn was largely abrogated (Figure 41). These data are consistent with the PAI-1:uPA complex having a significantly reduced affinity for Vn which permits the VNR receptor to displace the inactive complex. In contrast, uPA did not reduce the inhibition of ^{125}I-VNR binding to Vn by R346A PAI-1. This indicates that uPA enhances VNR binding by forming a complex with wtPAI-1 and is not due to proteolysis of either the VNR or Vn. A monoclonal antibody to $\alpha_v\beta_3$ (LM609) also inhibited the binding of ^{125}I-VNR to Vn to the same extent as did PAI-1 (Figure 41), confirming that this VNR preparation contained primarily $\alpha_V\beta_3$ and that PAI-1 blocks the binding of this integrin to Vn.

To see whether PAI-1 can inhibit the interaction of cellular integrins with Vn in a similar manner, attachment and migration assays using SMC were performed. Both active wtPAI-1 and R346A-PAI-1 inhibited SMC attachment to Vn (Figure 42A). In contrast, Q123K-PAI-1 had no affect on cell attachment, indicating that the inhibition of cell attachment by PAI-1 is due to its ability to bind Vn and not its inhibitory activity towards PAs. Furthermore, adding uPA to wtPAI-1 and Vn reversed the inhibition of cell attachment, whereas uPA had no affect on the inhibition of SMC attachment by R346A-PAI-1. Interestingly, PAI-1 is able to inhibit the attachment of SMC to Vn, while LM609 is not. This suggests that SMC have other integrins that can mediate attachment to Vn through the RGD integrin binding site and that PAI-1 blocks access of these integrins as well. Consistent with this interpretation a synthetic RGD containing peptide also blocked SMC attachment to Vn.

PAI-1 also inhibited the migration of SMC through Vn coated Transwells®. As observed with cell attachment, both active wtPAI-1 and R346A-PAI-1 prevented cell migration, whereas active Q123K-PAI-1 had no affect (Figure 42B). Inclusion of uPA negated the inhibition of migration by wtPAI-1 but not by R346A-PAI-1. This proved that, as with attachment, the inhibition of cell migration was due to PAI-1's capacity to bind Vn and not its inhibitory activity toward PAs. LM609, which did not prevent attachment,

inhibited migration, confirming that SMCs require $\alpha_v\beta_3$ for motility. These results are consistent with the observations that migrating vascular cells show elevated expression of both uPA and the VNR and that SMC show enhanced migration on Vn compared to other matrix proteins.

The results presented above suggest that SMC migration during normal wound healing requires both the cellular expression of $\alpha_v\beta_3$ and the presence of Vn in the matrix, and that PAI-1 may act as an important regulator of this process. However, subcellular matrices *in vivo* are much more complex, containing collagens, glycosaminoglycans, and other proteins such as laminin. Therefore, to examine the role of PAI-1 and Vn in cellular attachment and migration on such a heterogeneous matrix, and to see if PAI-1 could regulate this process, attachment and migration assays were performed on a complex basement membrane matrix derived from murine sarcoma cells (Matrigel®) in the presence or absence of Vn. Unlike cell attachment to purified Vn, PAI-1 had no affect on attachment to Matrigel even in the presence of Vn. This indicates that other proteins present in the matrix are support cell attachment, and, as was seen with fibronectin , PAI-1 had no affect on this association. PAI-1 also did not affect SMC migration through Matrigel-coated Transwells in the absence of added Vn. However, adsorption of Vn to the Matrigel markedly increased SMC migration (Figure 43). This is consistent with previous reports demonstrating that Vn significantly enhances migration of both SMC (Lawrence *et al.*, 1995, *supra;* Wilczynska *et al.*, *supra)* and primary keratinocytes (Aertgeets, K., *et al.* (1995) *Nature Structural Biology* 2, 891-897) and suggests that the presence of Vn in an exposed matrix or fibrin clot might stimulate cell migration. Furthermore, even though PAI-1 and LM609 had no affect on cell attachment to Matrigel containing Vn, they were able to inhibit cell migration on this complex matrix (Figure 43). As with purified Vn, the Q123K-PAI-1 had no effect on cell migration and the addition of uPA reversed the inhibition by wtPAI-1. Together, these results demonstrate that SMC migration on a complex matrix is enhanced by adsorption of Vn, and that this induction is $\alpha_v\beta_3$ dependent. PAI-1 can prevent this induction by blocking $\alpha_v\beta_3$ binding, and PAs can promote the induction by reversing the PAI-1 block. This

suggests that *in vivo*, the binding of plasma Vn to an exposed matrix following injury may act to accelerate cell migration during wound healing; and that PAI-1 may be an important factor regulating this process. Supporting this hypothesis, treatment of Matrigel coated Transwells with bovine serum enhanced SMC migration, in a PAI-1 inhibitable manner. These results are also consistent with the observation that PAI-1 null mice show enhanced SMC migration and proliferation, while in uPA-null mice SMC migration is reduced (Carmeliet, P. *et al.*, *Fibrinolysis 10 (Suppl. 3)*:19 (abstr 57) (1996)).

The specificity of the inhibition of integrin attachment to Vn by active PAI-1 further illustrates the unique functional interdependence that exists between PAI-1 and Vn. In addition to stabilizing PAI-1 in the active conformation, Vn also alters the specificity of PAI-1, making it an efficient inhibitor of thrombin, and promoting its clearance by members of the LDL receptor family. This suggests that thrombin, a known mitogen and chemotactic molecule, might also promote cell migration by removing PAI-1 from Vn. In addition, several studies have shown that both elastase and cathepsin G produced by activated neutrophils can efficiently remove PAI-1 from the matrix. Since PAI-1 is a substrate for these enzymes, only catalytic amounts are required to inactivate PAI-1. Together these findings indicate that a wide variety of proteinases are able to interact with PAI-1 and expose the RGD integrin binding site on Vn. This general ability to modify cellular adhesive properties by many divergent proteinases through a common mechanism suggests that the known correlation between increased cell migration and proteinase activity may be mediated, at least in part, by proteolytic interaction with PAI-1 in a wide variety of invasive cellular processes. It also suggests that the role of some proteinases in cellular migration may not be to cause generalized matrix degradation but instead maybe to expose cryptic cell attachment sites by inactivating PAI-1.

EXAMPLE VII

PAI-1 and Mutants in Cell Attachment, Migration, Angiogenesis and Clearance

The interactions between cells and their substrata is an important regulator of cellular function Signals from the extracellular matrix are conveyed to cell surface adhesion proteins such as members of the integrin family. Integrins bind to immobilized matrix proteins and help direct the cellular response to specific surface environments by mediating adhesion and/or migration. Cell migration is an important step in many physiological processes such as wound healing and angiogenesis and is also an important factor in pathological situations such as tumor progression and metastasis. Under normal conditions cell migration is a tightly controlled process which depends on the coordination of many factors (Lauffenburger, D.A. *et al.*, *Cell 84*:359-369 (1996)). Following injury the early matrix of a wound is primarily a cross-linked fibrin network associated with significant amounts of vitronectin. During wound healing, migrating cells, such as smooth muscle cells (SMC), endothelial cells and keratinocytes, exhibit an increased expression of the vitronectin receptor (VNR) integrins including $\alpha_V\beta_3$ and $\alpha_V\beta_5$ (Liaw, L. *et al.*, *J Clin Invest 95*:713-724 (1995); Liaw *et al.*, *Circ Res 77*:665-672 (1995); Brooks *et al.*, 1994, *supra*; Brooks, P.C. *et al.*, *Cell 79*:1157-1164 (1994)). The integrin $\alpha_V\beta_3$ has also been shown to be transiently expressed at the leading edge of cells invading a fibrin clot (Clark R.A.F. *et al.*, *Am J Pathol 148*:1407-1421 (1996)). This association between VNR expression and cellular migration has led to the suggestion that the $\alpha_V\beta_3$ integrin is important for cell motility.

The present inventors have shown that $\alpha_V\beta_3$ is not required for smooth muscle cell attachment to Vn but is required for cell motility (Example VI). It was also demonstrated that the $\alpha_V\beta_3$ attachment site on Vn overlaps with the binding site for PAI-1 and that the active conformation of PAI-1 blocks the attachment and migration of vascular SMCs on Vn.. This effect is not dependent on PAI-1's ability to inhibit plasminogen activators (PAs) but does require high affinity binding to Vn. Complex formation between PAs and PAI-1 results in loss of PAI-1 affinity for Vn and restores cell attachment and migration. These data demonstrate that

PAI-1 can control cell-matrix interactions by regulating the accessibility of specific cell attachment sites and suggests that the localization of PA activity at sites of focal contact is not to initiate a proteolytic cascade leading to generalized matrix destruction, but instead is required to expose cryptic cell attachment sites on Vn necessary for smooth muscle cell migration.

Figures 44 and 45 show that the SMC migration is affected both by the concentration of Vn which is adsorbed to the Transwell migration chamber (Figure 44) and that PAI-1 is a more efficient inhibitor of SMC migration at lower Vn coating concentration (Figure 45). Since Vn in plasma is thought to bind to extravascular matrix upon injury, experiments were done to test whether Vn from serum showed similar effects. Shown in Figure 47 is the migration of SMC on Transwell filters coated first with Matrigel and then exposed to either purified native Vn or bovine serum. Consistent with our previous observations, SMC migrated faster on Matrigel in the presence of Vn. Serum also stimulated the migration of SMC which were inhibited by the addition of PAI-1. This shows that serum Vn has the same ability as purified native Vn to accelerate SMC migration and that PAI-1 is able to inhibit this interaction as well.

The ability of PAI-1 to block the binding of cellular integrins to Vn is probably due to the fact that PAI-1 has a greater affinity for Vn than do integrins. Shown in Figure 47 is a comparison of the ability of PAI-1 to inhibit SMC attachment compared to a peptide containing the RGD sequence and to mAb to $\alpha_v\beta_3$ (LM609) The RGD-containing peptide but not a corresponding RGE-containing peptide inhibited all SMC attachment to Vn. Antibody LM609 did not inhibit SMC attachment, consistent with the fact that these cells have other Vn specific integrins. PAI-1, like the RGD containing peptide, could inhibit all SMC attachment to Vn. However it had similar efficacy at approximately a 100 fold lower concentration.

In processes such as wound healing and angiogenesis, SMC act in concert with endothelial cells to seal a wound and to produce a functioning capillary vessel. To evaluate the use of PAI-1 in these processes, studies were done examining the effect of PAI-1 on endothelial cell attachment to Vn using bovine aortic endothelial cells (BAE). Figures 48 and 49A-49B show that PAI-1 was unable to inhibit the

attachment of BAE to Vn to the same extent as the RGD-containing peptide. A possible explanation is that endothelial cells having other RGD binding integrins that are able to recognize other sites on Vn, distal to the from the normal cell attachment site and the PAI-1 binding site. In addition to blocking SMC migration *in vitro*, PAI-1 also blocked cytokine-induced angiogenesis *in vivo* (Figures 50A-50C). These results were obtained using the stabilized 14-1B mutant which has four amino acid substitutions compared to wild-type (N150H, K154T, Q319L, M354I). These results show that this stabilized PAI-1 and additional PAI-1 mutants inhibit angiogenesis in the chicken chorioallantoic membrane (CAM). At least part of the inhibition is due to blocking Vn accessibility.

Apart from PAI-1-mediated inhibition of cell attachment and migration, which is dependent on high affinity binding to Vn, other uses of PAI-1 mutants exploit the high affinity that PAI-1 has for clearance receptors upon complex formation with proteinase. PAI-1 proteinase complexes show higher affinity for the clearance receptors LRP and gp330 than other serpin enzyme complexes tested. Shown in Figure 51 is the cell mediated degradation of ^{125}I-neutrophil elastase by either PAI-1 elastase inhibitor mutant (R346A) compared to the natural proteinase inhibitor α1-proteinase inhibitor. This elevated degradation occurs via endosomes and lysosomes since it is inhibited by chloroquine.

Since neutrophil elastase prefers to cleave at the C-terminal side of valine, the present inventors examined whether the efficiency of elastase inhibition by PAI-1 could be improved by introducing a valine residue in the reactive center bond. Additionally it was desired to eliminate valine at position 343, an elastase-sensitive site in wtPAI-1 that leads to inactivation of PAI-1. Shown in Figure 52 is a comparison of the inhibition of elastase by various PAI-1 mutants and by α1-proteinase inhibitor. As can be seen in this figure the PAI-1 containing valine at 346 (R346V) and alanine at position 343 (V343A) is a more efficient inhibitor of elastase than other PAI-1 mutants tested.

The references cited above are all incorporated by reference herein, whether specifically incorporated or not.

Having now fully described this invention, it will be appreciated by those skilled in the art that the same can be performed within a wide range of equivalent parameters, concentrations, and conditions without departing from the spirit and scope of the invention and without undue experimentation.

While this invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth as follows in the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LAWRENCE, DANIEL A.
STEFANSSON, STEINGRIMUR P.

(ii) TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
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(F) ZIP: 20006-1812

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: LIVNAT, SHMUEL
(B) REGISTRATION NUMBER: 33,949
(C) REFERENCE/DOCKET NUMBER: 30807-20004.00

(ix) TELECOMMUNICATION INFORMATION:
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(B) TELEFAX: (202) 822-0168
(C) TELEX: 90-4030 MRSNFOERSWSH

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 76..1281

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 145

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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1791

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1971

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2031

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2271

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2331

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2391

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2451

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly
1 5 10 15

Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val
20 25 30

Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu
35 40 45

Thr Thr Gly Gly Glu Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe
50 55 60

Lys Ile As[illegible]sp Lys Gly Met Ala Pro Ala Leu Arg [illegible] Leu Tyr Lys

```
65                  70                  75                  80
Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala
                85                  90                  95
Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro His
            100                 105                 110
Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu
        115                 120                 125
Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr
    130                 135                 140
Lys Gly Met Ile Ser Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu
145                 150                 155                 160
Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys
                165                 170                 175
Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys Ser
            180                 185                 190
Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe
        195                 200                 205
Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu
    210                 215                 220
Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro
225                 230                 235                 240
Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala
                245                 250                 255
Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu
            260                 265                 270
Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys
        275                 280                 285
Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala
    290                 295                 300
Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala
305                 310                 315                 320
Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser
                325                 330                 335
Ser Ser Thr Ala Val Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile
            340                 345                 350
Ile Met Asp Arg Pro Phe Leu Phe Val Val Arg His Asn Pro Thr Gly
        355                 360                 365
Thr Val Leu Phe Met Gly Gln Val Met Glu Pro
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7[illegible] amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Met Ile Thr Asn Ser
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCTCAGCCG CCATGGCCCC C
21

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCTCAGCCG TCATGGCCCC C
21

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGTCATAG CCTCAGCCCG C
21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTGTCATAG CCTCAGCCGT CATGGCCCCC
30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) S' NDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGTCATAG CCTCAGCCGC CATGGCCCCC
30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTTCTATTA GATTACATTC ATTTCACATC TGTGTGCAAT TCTCCCATAA ATTGGTCTTT
60

AAAATATATA TATATATTTA AAGATATTAG AAATATATAT TTAAGTATAT TTAAAATATA
120

TATATTTTTA AAGAGACGGG GGTCTTGGTA TGTTGCCCAG GCTGGTCTTG AACTCCTGGG
180

CTCAAGCAAT CCTCCCGCCT TGGCCTCCCA AAGTGCATTA CATCCATCTT TGTGCCCTAC
240

CCTCTGGCTG GTAGGTTTTC AGAAATATTA TCTAAGGTAG TTGAATCCGA GCTGCCTGTC
300

TCTCTCACCC ACCCCCCCCT CACGTGTCCA CTGCTCACAC ACAGCAGCCG GAAATGACAC
360

ATTGAAGTGA GTCACCAATG CGGCTGTGAG TCACCCTGTA ATTGGGGAAA GTTCTGTCCT
420

GGTAGGTCAT GCAGCCCCTT GCATTTCTGC TCCTAAATCT ATTGAACACA TTGGAAACCA
480

CTCTGTCCTC ATCTGAGTCT CTGTCCCCCC ACTCCGTCCT TTTGATCCCC TGAAGGAGGA
540

TGAAATTGTA TGGTCAATTT CCATCAAGGG GAAAAAGAGG GGCGCGGGGG GCGCGGGGGG
600

CGCGAGGGTC TCAGGCGGCC ACAAGGTGGC AGTGTGGGCT CCGTCACGCT GGATGTCCGG
660

AGGGGTGTGT GCCAGTCAAG TGGCTGGACT TCCTGAGATA CGGTGACACA GACCACAAAG
720

AAACACTAGG AGCGAGTTTA AATAATATTA TTTTCCTTAG TAGTTCTCTT TGTCTCTAAC
780

AAGCACTCAA GGGCAAGGAT ATGATAAATA TTTAGGTACA CCCCTCCCCA CCAAGAGATT
840

GGGGGGTGAA GAGCTGGGCA CGCATCTGAC ATTTCTTCCT CTATTCCTAT AAAAATAAAA
900

GGAAGCAGAA ATCTGCTTCA ATGAGTAAAC AAGTCACGTA CAGTCCAAAA TAACCCATGC
960

ACACTGTTTC TGGGGAGGGA GATGGCCAGG CCAGGAGAGT TGGGCCACAT GATGGGGGAC
1020

ATTCACTCTG CCACCTGCAG CACCCCTGTA CTGGGGAGGG GTGGCCAGTG GCACAGTGGA
1080

CTCTGAGATG AAAGGGTGTT TCTTCCACTG GCCTTTGGCC TGTCACCAGC CTCCTCCGCG
1140

GTGGCAGGCA GTACAAGAGT GATGGCAATG TGACTGGAAC AGAAATAGTT TCTACCAGGC
1200

ACACAAAAGC TCCTGTAAGC CCCGTAGTTC CATCCTGCAA AGGGCCTCAG TGGGAACCAG
1260

GTCTGCAGAC CCGAGTGGGC AGAGAGACGG GTGGAAGCAG GTGCCCCAGA TGGTCCCGCA
1320

GGCGTCACCG TCTGGTTTGG AGACCTTAAG GGAGTTGTGC TTCAAACTTC TCTCCCAGGG
1380

TCTCAGGTGG AGACTAGGGA GTTTGACCTA AAGGTCCTCC AAGGAGAGGC CAAGGTCTTG
1440

GAGACAGATC TGGTTTACCA TCTTTTAACA AAAGGCAAAT GTCTTCTGTT CCTTCAGAAA
1500

GAGTCATTAA CACTAAAATT CTTTTCTTCG GAGTTTCTTC TTTCGCGATG GATCTCCAGT
1560

TTTGTCCCAG ATGAAGGCGT CTTTCCCCAG GGTCAGGGTT CCATCACTTG GCCCATGAAA
1620

AGGACTGTTC CTGTGGGGTT GTGCCGGACC ACAAAGAGGA AGGGTCTGTC CATGATGATC
1680

TCCTCGGGGG CCATGCGGGC TGAGACTATG ACAGCTGTGG ATGAGGAGGC CACCGTGCCA
1740

CTCTCGTTCA CCTCGATCTT CACTTTCTGC AGCGCCTGCG CGACGTGGAG AGGCTCTTGG
1800

TCTGAAAGAC TCGTGAAGTC AGCCTGAAAC TGTCTGAACA TGTCGGTCAT TCCCAGGTTC
1860

TCTAGGGGCT TCCTGAGGTC GACTTCAGTC TCCAGGGAGA ACTTGGGCAG AACCAGGAGG
1920

CGGGGCAGCC TGGTCATGTT GCCTTTCCAG TGGCTGATGA GCTGGGCACT CAGAATGTTG
1980

GTGAGGGCAG AGAGAGGCAC CTCTTTTTCA TAAGGGGCAG CAATGAACAT GCTGAGGGTG
2040

TCCCCGTGGT AGGGCAGTTC CAGGATGTCG TAGTAATGGC CATCGGGCGT GGTGAACTCA
2100

GTATAGTTGA ACTTGTTGGT CTGAGCCATC ATGGGCACAG AGACAGTGCT GCCGTCTGAT
2160

TTGTGGAAGA GGCGGCGGTG GGTGCTGGAG TCGGGGAAGG GAGTCTTCCA CTGGCCGTTG
2220

AAGTAGAGGG CATTCACCAG CACCAGCCGT GTCAGCTGGT GCACGGCTCC TTTCCCAAGC
2280

AAGTTGCTGA TCATACCTTT TGTGTGTGTC TTCACCCAGT CATTGATGAT GAATCTGGCT
2340

CTCTCCACCT CTGAAAAGTC CACTTGCTTG ACCGTGCTCC GGAACAGCCT GAAGAAGTGG
2400

GGCATGAAGC CCTGGACCAG CTTCAGATCG CGCTGGACGA AGATCGCGTC TGTGGTGCTG
2460

ATCTCATCCT TGTTCCATGG CCCCATGAGC TCCTTGTACA GATGCGGGAG GGCGGGGGCC
2520

ATGCCCTTGT CATCAATCTT GAATCCCATA GCTGCTTGAA TCTGCTGCTG GGTTTCTCCT
2580

CCTGTTGTCA GCTGGAGCAT GGCCAAGACC GAGGCCACCC CATAGGGTGA GAAAACCACG
2640

TTGCGGTCCT TGGAGGCCTG CGCCACCTGC TGAAACACCC TCACCCCGAA GTCTGAGGCC
2700

AGGTGGGCCA CGTAGGATGG GGGATGGTGC ACAGCAGACC CTTCACCAAA GACAAGGGCC
2760

AGGCCCAGGA CTAGGCAGGT GAGGGCTGGA GACATCTGCA TCCTGAAGTT CTCAGAGGTG
2820

CCTTGCGATT GGCGGTTCGT CCTGCTCTGG CGGCGGCTGC TGAGCTGCAG GAATTC
2876

WHAT IS CLAIMED IS:

1. A mutant protein of PAI-1 protein, the wild type sequence of which is SEQ ID NO:3, which mutant inhibits neutrophil elastase or other elastase-like proteinases.

2. A mutant protein according to claim 1 which inhibits said elastase activity such that no more than about ten moles of said mutant protein is required to inhibit 1 mole of said elastase.

3. A mutant protein according to claim 1 which has at least one amino acid substitution in the sequence from position 343 to 350 of SEQ ID NO:3.

4. A mutant protein according to claim 3, wherein said substitution is

(a) at position 343 and selected from the group consisting of Ala, Asp, Gly, Leu and Ile;

(b) at position 346 and selected from the group consisting of Ala, Val, Asp, Phe and Gly; or

(c) both (a) and (b).

5. A mutant protein according to claim 4, which differs from SEQ ID NO:3 by a single substitution of Val at position 346, a single substitution of Ala at position 343 or both Val at position 346 and Ala at position 343.

6. A mutant protein according to claim 5, wherein the amino acid substituting at position 343:

(a) renders said mutant protein resistant to cleavage by elastase at sites C-terminal to position 343, and

(b) has a side chain which does not interfere with the binding of said mutant protein to said elastase to form a mutant PAI-1:elastase complex.

7. A mutant protein according to claim 3 which further comprises between one and four of the following additional amino acid substitutions in SEQ ID NO:3:

(a) His at position 150;

(b) Thr at position 154;

(c) Leu at position 319; and

(d) Ile at position 354.

8. A mutant protein according to claim 3 which further comprises one or more of the following substitutions in SEQ ID NO:3:

(a) Arg at position 333; and

(b) Arg at position 335;

(c) Gly at position 331;

(d) Ile at position 372; and

(d) Leu at position 91.

9. A mutant protein of PAI-1 protein the wild type sequence of which is SEQ ID NO:3, which mutant is characterized by being resistant to inactivation by the following proteinases: elastase, a plasminogen activator, plasmin, thrombin, cathepsin G, chymase, gelatinase A, gelatinase B, stromelysin and collagenase

10. A mutant protein of PAI-1 protein the wild type sequence of which is SEQ ID NO:3 which mutant is characterized by having high affinity for vitronectin such that the binding of said mutant protein to a proteinase does not decrease the affinity of binding of said mutant protein to vitronectin more than about 100-fold relative to the affinity of wild-type PAI-1 to vitronectin.

11. A mutant protein according to claim 10 which has at least one amino acid substitution in the sequence from position 331 to 350 of SEQ ID NO:3.

12. A mutant protein according to claim 10 which is has between one and four of the following additional amino acid substitutions in SEQ ID NO:3:

(a) His at position 150;

(b) Thr at position 154;

(c) Leu at position 319; and

(d) Ile at position 354.

13. A mutant protein according to claim 12 which further comprises one or both of the following substitutions:

(a) Arg at position 333;

(b) Arg at position 335.

(c) Gly at position 331;

(d) Ile at position 372; and

(e) Leu at position 91.

14. A mutant protein of PAI-1 protein which has a higher affinity for vitronectin than does wild-type PAI-1.

15. A pharmaceutical composition useful for inhibiting elastase activity in a subject, comprising:

(a) a mutant protein according to claim 1; and

(b) a pharmaceutically acceptable carrier or excipient.

16. A pharmaceutical composition useful for inhibiting elastase activity in a subject, comprising:

(a) a mutant protein according to claim 3; and

(b) a pharmaceutically acceptable carrier or excipient.

17. A pharmaceutical composition useful for inhibiting elastase activity in a subject, comprising:

(a) a mutant protein according to claim 7; and

(b) a pharmaceutically acceptable carrier or excipient.

18 A pharmaceutical composition useful for inhibiting vitronectin-dependent cell attachment, migration and/or migration-induced cell proliferation in a subject, comprising

(a) a mutant protein according to claim 10 and

(b) a pharmaceutically acceptable carrier or excipient.

19. A pharmaceutical composition useful for inhibiting vitronectin-dependent cell attachment, migration and/or migration-induced cell proliferation in a subject, comprising

(a) a mutant protein according to claim 11; and

(b) a pharmaceutically acceptable carrier or excipient.

20. A pharmaceutical composition useful for inhibiting vitronectin-dependent cell attachment, migration and/or migration-induced cell proliferation in a subject, comprising

(a) a mutant protein according to claim 13; and

(b) a pharmaceutically acceptable carrier or excipient.

21. A method for inhibiting elastase in a subject having a disease or condition associated with pathogenic elastase activity, comprising administering to said subject an effective amount of a pharmaceutical composition according to claim 15.

22. A method according to claim 21 wherein said disease or condition is selected from the group consisting of emphysema, acute respiratory distress syndrome, acute inflammatory lung injury, congenital alpha-1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, pancreatitis, periodontal disease, arthritis and HIV infection.

23. A method for inhibiting cell attachment, migration and/or migration-induced cell proliferation in a subject having a disease or condition associated with undesired vitronectin-dependent cell attachment, migration or migration-induced proliferation, comprising administering to said subject an effective amount of

(a) a pharmaceutical composition comprising wild type PAI-1 protein and a pharmaceutically acceptable carrier or excipient; or

(b) a pharmaceutical composition according to claim 18.

24. A method according to claim 23 wherein said disease or condition is atherosclerosis, post-balloon angioplasty vascular restenosis, neointima formation following vascular trauma, vascular graft restenosis, fibrosis associated with a chronic inflammatory condition, lung fibrosis, chemotherapy-induced fibrosis, wound healing with scarring and fibrosis, primary tumor growth, invasion or growth of a tumor metastasis, psoriasis, deep venous thrombosis, or a disease or condition in which angiogenesis is pathogenic.

25. A nucleic acid molecule encoding a mutant PAI-1 protein according to claim 1.

26. A nucleic acid molecule according to claim 25 which is a variant of SEQ ID NO:1 or of a coding portion thereof.

27. A nucleic acid molecule encoding a mutant PAI-1 protein according to claim 10.

28. A nucleic acid molecule according to claim 27 which is a variant of SEQ ID NO:1 or of a coding portion thereof.

29. A host cell transformed or transfected with a molecule according to claim 25.

30. A host cell transformed or transfected with a molecule according to claim 27.

31. An antibody specific for an epitope of a mutant PAI-1 protein of claim 1, which epitope is not present on wild-type PAI-1.

32. An antibody specific for an epitope of a mutant PAI-1 protein of claim 10, which epitope is not present on wild-type PAI-1.

Active Form

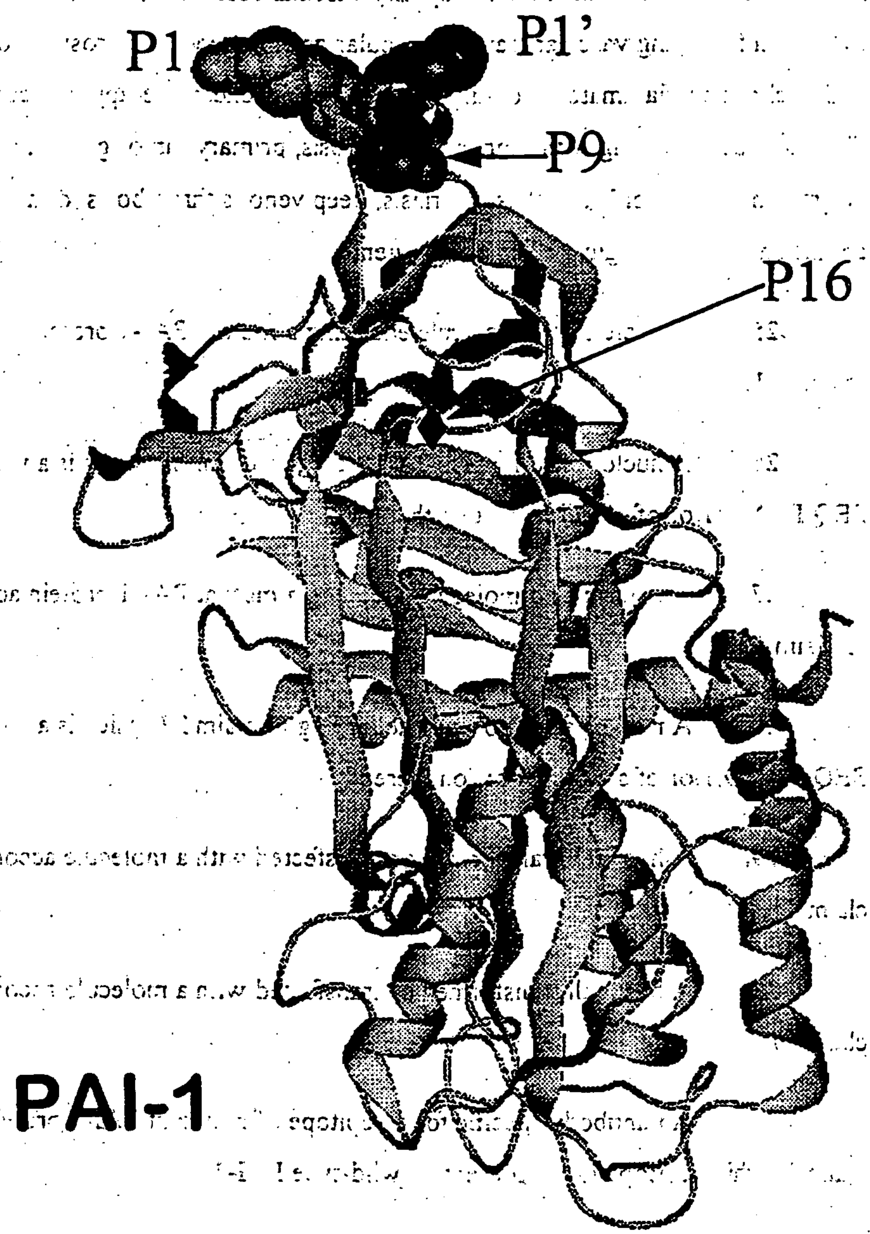


Fig. 1

Inactive (Cleaved) Form

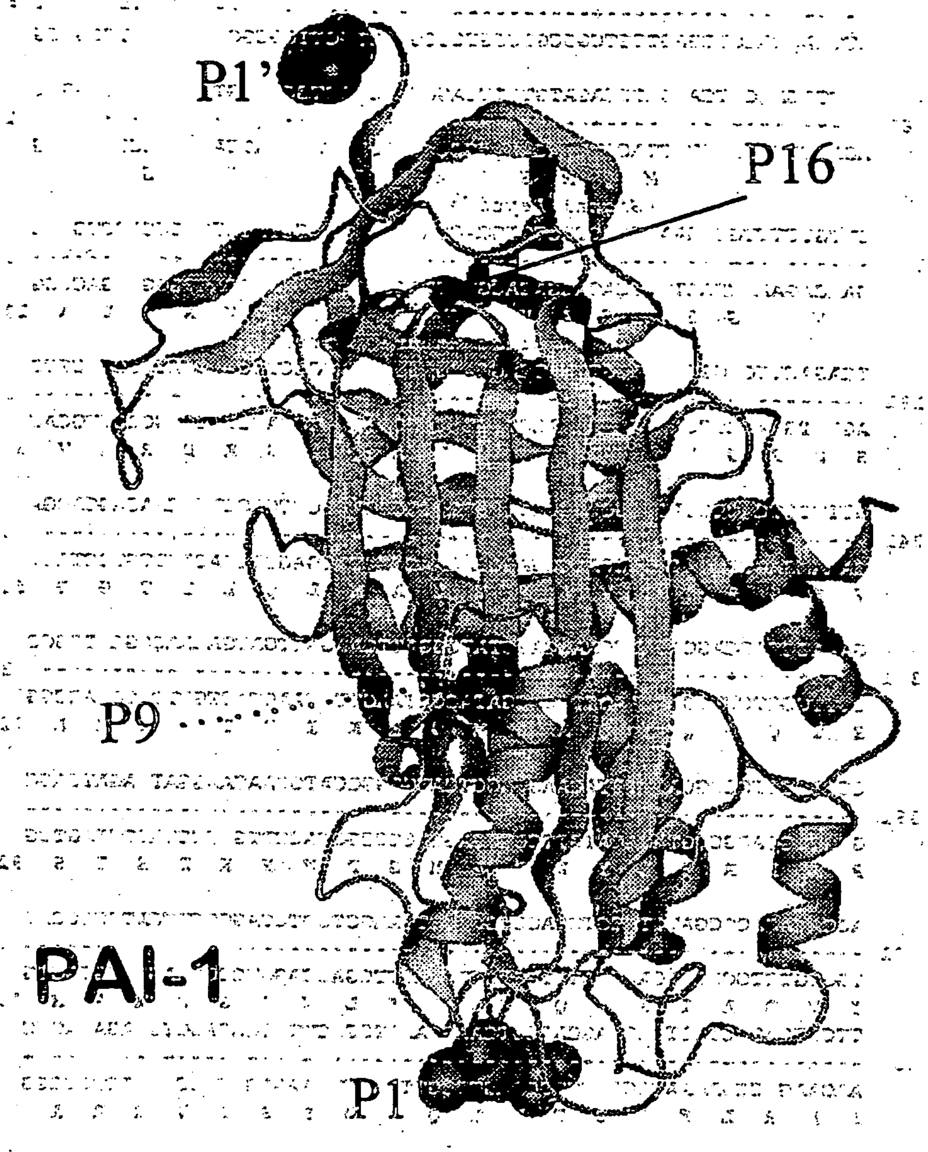


Fig. 2

Nucleotide (SEQ ID NO:1) and Amino Acid (SEQ ID NO:2)
Sequences of Human Plasminogen Activator Inhibitor-1 (PAI-1)

[*Signal Peptide* in italics and **Mature Protein** in bold]

```
        GAATTCCTGCAGCTCAGCAGCCGCCGCCAGAGCAGGACGAACCGCCAATCGCAAGGCACC
      1 ---------+---------+---------+---------+---------+---------+ 60
        CTTAAGGACGTCGAGTCGTCGGCGGCGGTCTCGTCCTGCTTGGCGGTTAGCGTTCCGTGG

        TCTGAGAACTTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCTGGCC
     61 ---------+---------+---------+---------+---------+---------+ 120
        AGACTCTTGAAGTCCTACGTCTACAGAGGTCGGGAGTGGACGGATCAGGACCCGGACCGG
aa                    M  Q  M  S  P  A  L  T  C  L  V  L  G  L  A  -
                     |Signal Peptide
        CTTGTCTTTGGTGAAGGGTCTGCTGTGCACCATCCCCCATCCTACGTGGCCCACCTGGCC
    121 ---------+---------+---------+---------+---------+---------+ 180
        GAACAGAAACCACTTCCCAGACGACACGTGGTAGGGGGTAGGATGCACCGGGTGGACCGG
aa       L  V  F  G  E  G  S  A |V  H  H  P  P  S  Y  V  A  H  L  A  12
                                 Start Mature Protein
        TCAGACTTCGGGGTGAGGGTGTTTCAGCAGGTGGCGCAGGCCTCCAAGGACCGCAACGTG
    181 ---------+---------+---------+---------+---------+---------+ 240
        AGTCTGAAGCCCCACTCCCACAAAGTCGTCCACCGCGTCCGGAGGTTCCTGGCGTTGCAC
aa       S  D  F  G  V  R  V  F  Q  Q  V  A  Q  A  S  K  D  R  N  V  32

        GTTTTCTCACCCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA
    241 ---------+---------+---------+---------+---------+---------+ 300
        CAAAAGAGTGGGATACCCCACCGGAGCCACAACCGGTACGAGGTCGACTGTTGTCCTCCT
aa       V  F  S  P  Y  G  V  A  S  V  L  A  M  L  Q  L  T  T  G  G  52

        GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC
    301 ---------+---------+---------+---------+---------+---------+ 360
        CTTTGGGTCGTCGTCTAAGTTCGTCGATACCCTAAGTTCTAACTACTGTTCCCGTACCGG
aa       E  T  Q  Q  Q  I  Q  A  A  M  G  F  K  I  D  D  K  G  M  A  72

        CCCGCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC
    361 ---------+---------+---------+---------+---------+---------+ 420
        GGGCGGGAGGCCGTAGACATGTTCCTCGAGTACCCCGGTACCTTGTTCCTACTCTAGTCG
aa       P  A  L  R  H  L  Y  K  E  L  M  G  P  W  N  K  D  E  I  S  92

        ACCACAGACGCGATCTTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCAC
    421 ---------+---------+---------+---------+---------+---------+ 480
        TGGTGTCTGCGCTAGAAGCAGGTCGCCCTAGACTTCGACCAGGTCCCGAAGTACGGGGTG
aa       T  T  D  A  I  F  V  Q  R  D  L  K  L  V  Q  G  F  M  P  H  112
        TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCC
    481 ---------+---------+---------+---------+---------+---------+ 540
        AAGAAGTCCGACAAGGCCTCGTGCCAGTTCGTTCACCTGAAAAGTCTCCACCTCTCTCGG
aa       F  F  R  L  F  R  S  T  V  K  Q  V  D  F  S  E  V  E  R  A  132

        AGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTT
    541 ---------+---------+---------+---------+---------+---------+ 600
        TCTAAGTAGTAGTTACTGACCCACTTCTGTGTGTGTTTTCCATACTAGTCGTTGAACGAA
aa       R  F  I  I  N  D  W  V  K  T  H  T  K  G  M  I  S  N  L  L  152
```

Fig. 3 (sheet 1/4)

```
      GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGTGAATGCCCTCTACTTCAAC
 601  ---------+---------+---------+---------+---------+---------+ 660
      CCCTTTCCTCGGCACCTGGTCGACTGTGCCGACCACGACCACTTACGGGAGATGAAGTTG
aa     G  K  G  A  V  D  Q  L  T  R  L  V  L  V  N  A  L  Y  F  N  172

      GGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCCTCTTCCACAAATCA
 661  ---------+---------+---------+---------+---------+---------+ 720
      CCGGTCACCTTCTGAGGGAAGGGGCTGAGGTCGTGGGTGGCGGCGGAGAAGGTGTTTAGT
aa     G  Q  W  K  T  P  F  P  D  S  S  T  H  R  R  L  F  H  K  S  192

      GACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
 721  ---------+---------+---------+---------+---------+---------+ 780
      CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
aa     D  G  S  T  V  S  V  P  M  M  A  Q  T  N  K  F  N  Y  T  E  212

      TTCACCACGCCCGATGGCCATTACTACGACATCCTGGAACTGCCCTACCACGGGGACACC
 781  ---------+---------+---------+---------+---------+---------+ 840
      AAGTGGTGCGGGCTACCGGTAATGATGCTGTAGGACCTTGACGGGATGGTGCCCCTGTGG
aa     F  T  T  P  D  G  H  Y  Y  D  I  L  E  L  P  Y  H  G  D  T  232

      CTCAGCATGTTCATTGCTGCCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAAC
 841  ---------+---------+---------+---------+---------+---------+ 900
      GAGTCGTACAAGTAACGACGGGGAATACTTTTTCTCCACGGAGAGAGACGGGAGTGGTTG
aa     L  S  M  F  I  A  A  P  Y  E  K  E  V  P  L  S  A  L  T  N  252

      ATTCTGAGTGCCCAGCTCATCAGCCACTGGAAAGGCAACATGACCAGGCTGCCCCGCCTC
 901  ---------+---------+---------+---------+---------+---------+ 960
      TAAGACTCACGGGTCGAGTAGTCGGTGACCTTTCCGTTGTACTGGTCCGACGGGGCGGAG
aa     I  L  S  A  Q  L  I  S  H  W  K  G  N  M  T  R  L  P  R  L  272

      CTGGTTCTGCCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCTAGAGAAC
 961  ---------+---------+---------+---------+---------+---------+ 1020
      GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTTCGGGGATCTCTTG
aa     L  V  L  P  K  F  S  L  E  T  E  V  D  L  R  K  P  L  E  N  292

      CTGGGAATGACCGACATGTTCAGACAGTTTCAGGCTGACTTCAGGAGTCTTTCAGACCAA
1021  ---------+---------+---------+---------+---------+---------+ 1080
      GACCCTTACTGGCTGTACAAGTCTGTCAAAGTCCGACTGAAGTCCTCAGAAAGTCTGGTT
aa     L  G  M  T  D  M  F  R  Q  F  Q  A  D  F  R  S  L  S  D  Q  312

      GAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
1081  ---------+---------+---------+---------+---------+---------+ 1140
      CTCGGAGAGGTGCAGCGCGTCCGCGACGTCTTTCACTTCTAGCTCCACTTGCTCTCACCG
aa     E  P  L  H  V  A  Q  A  L  Q  K  V  K  I  E  V  N  E  S  G  332

      ACGGTGGCCTCCTCATCCACAGCTGTCATAGTCTCAGCCCGCATGGCCCCCGAGGAGATC
1141  ---------+---------+---------+---------+---------+---------+ 1200
      TGCCACCGGAGGAGTAGGTGTCGACAGTATCAGAGTCGGGCGTACCGGGGGCTCCTCTAG
aa     T  V  A  S  S  S  T  A  V  I  V  S  A  R  M  A  P  E  E  I  352

      ATCATGGACAGACCCTTCCTCTTTGTGGTCCGGCACAACCCCACAGGAACAGTCCTTTTC
1201  ---------+---------+---------+---------+---------+---------+ 1260
      TAGTACCTGTCTGGGAAGGAGAAACACCAGGCCGTGTTGGGGTGTCCTTGTCAGGAAAAG
aa     I  M  D  R  P  F  L  F  V  V  R  H  N  P  T  G  T  V  L  F  372
```

Fig. 3 (sheet 2/4)

```
     ATGGGCCAAGTGATGGAACCCTGACCCTGGGGAAAGACGCGTTCATCTGGGACAAAACTG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TACCCGGTTCACTACCTTGGGACTGGGACCCCTTTCTGCGGAAGTAGACCCTGTTTTGAC
a a   M  G  Q  V  M  E  P  * 379

     GAGATGCATCGGGAAAGAAGAAACTCCGAAGAAAAGAATTTTAGTGTTAATGACTCTTTC
1321 ---------+---------+---------+---------+---------+---------+ 1380
     CTCTACGTAGCCCTTTCTTCTTTGAGGCTTCTTTTCTTAAAATCACAATTACTGAGAAAG

     TGAAGGAAGAGAAGACATTTGCCTTTTGTTAAAAGATGGTAAACCAGATCTGTCTCCAAG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     ACTTCCTTCTCTTCTGTAAACGGAAAACAATTTTCTACCATTTGGTCTAGACAGAGGTTC

     ACCTTGGCCTCTCCTTGGAGGACCTTTAGGTCAAACTCCCTAGTCTCCACCTGAGACCCT
1441 ---------+---------+---------+---------+---------+---------+ 1500
     TGGAAGCGGAGAGGAACCTCCTGGAAATCCAGTTTGAGGGATCAGAGGTGGACTCTGGGA

     GGGAGAGAAGTTTGAAGCACAACTCCCTTAAGGTCTCCAAACCAGACGGTGACGCCTGCG
1501 ---------+---------+---------+---------+---------+---------+ 1560
     CCCTCTCTTCAAACTTCGTGTTGAGGGAATTCCAGAGGTTTGGTCTGCCACTGCGGACGC

     GGACCATCTGGGGCACCTGCTTCCACCCGTCTCTCTGCCCACTCGGGTCTGCAGACCTGG
1561 ---------+---------+---------+---------+---------+---------+ 1620
     CCTGGTAGACCCCGTGGACGAAGGTGGGCAGAGAGACGGGTGAGCCCAGACGTCTGGACC

     TTCCCACTGAGGCCGTTTGCAGGATGGAACTACGGGGCTTACAGGAGCTTTTGTGTGCCT
1621 ---------+---------+---------+---------+---------+---------+ 1680
     AAGGGTGACTCCGGGAAACGTCCTACCTTGATGCCCCGAATGTCCTCGAAAACACACGGA

     GGTAGAAACTATTTCTGTTCCAGTCACATTGCCATCACTCTTGTACTGCCTGCCACCGCG
1681 ---------+---------+---------+---------+---------+---------+ 1740
     CCATCTTTGATAAAGACAAGGTCAGTGTAACGGTAGTGAGAACATGACGGACGGTGGCGC

     GAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAGAAACACCCTTTCATCTCAGAGTCCA
1741 ---------+---------+---------+---------+---------+---------+ 1800
     CTCCTCCGACCACTGTCCGGTTTCCGGTCACCTTCTTTGTGGGAAAGTAGAGTCTCAGGT

     CTGTGGCACTGGCCACCCCTGCCGAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCC
1801 ---------+---------+---------+---------+---------+---------+ 1860
     GACACCGTGACCGGTGGGGACGGCTCATGTCCCCACGACGTCCACCGTCTCACTTACAGG

     CCCATCATGTGGCCCAACTCTCCTGGCCTGGCCATCTCCCTCCCCAGAAACAGTGTGCAT
1861 ---------+---------+---------+---------+---------+---------+ 1920
     GGGTAGTACACCGGGTTGAGAGGACCGGACCGGTAGAGGGAGGGGTCTTTGTCACACGTA

     GGGTTATTTTGGAGTGTAGGTGACTTGTTTACTCATTGAAGCAGATTTGTGGTTCCTTTT
1921 ---------+---------+---------+---------+---------+---------+ 1980
     CCCAATAAAACCTCACATCCACTGAACAAATGAGTAACTTCGTCTAAACACCAAGGAAAA

     ATTTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCCAGCTCTTCACCCCCCAATC
1981 ---------+---------+---------+---------+---------+---------+ 2040
     TAAAAATATCCTTATCTCCTTCTTTACAGTCTACGCACGGGTCGAGAAGTGGGGGGTTAG
```

Fig. 3 (sheet 3/4)

```
     TCTTGGTGGGGAGGGGTGTACCTAAATATTTATCATATCCTTGCCCTTGAGTGCTTGTTA
2041 ---------+---------+---------+---------+---------+---------+ 2100
     AGAACCACCCCTCCCCACATGGATTTATAAATAGTATAGGAACGGGAACTCACGAACAAT

     GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTTAAACTCGCTCCTAGTGTTTCTTT
2101 ---------+---------+---------+---------+---------+---------+ 2160
     CTCTCTTTCTCTTGATGATTCCTTTTATTATAATAAATTTGAGCGAGGATCACAAAGAAA

     GTGGTCTGTGTCACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGG
2161 ---------+---------+---------+---------+---------+---------+ 2220
     CACCAGACACAGTGGCATAGAGTCCTTCAGGTCGGTGAACTGACCGTGTGTGGGGAGGCC

     ACATCCAGCGTGACGGAGCCCACACTGCCACCTTGTGGCCGCCTGAGACCCTCGCGCCCC
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TGTAGGTCGCACTGCCTCGGGTGTGACGGTGGAACACCGGCGGACTCTGGGAGCGCGGGG

     CCGCGCCCCCCGCGCCCCTCTTTTTCCCCTTGATGGAAATTGACCATACAATTTCATCCT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     GGCGCGGGGGGCGCGGGGAGAAAAAGGGGAACTACCTTTAACTGGTATGTTAAAGTAGGA

     CCTTCAGGGGATCAAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGGT
2341 ---------+---------+---------+---------+---------+---------+ 2400
     GGAAGTCCCCTAGTTTTCCTGCCTCACCCCCCTGTCTCTGAGTCTACTCCTGTCTCACCA

     TTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGA
2401 ---------+---------+---------+---------+---------+---------+ 2460
     AAGGTTACACAAGTTATCTAAATCCTCGTCTTTACGTTCCCCGACGTACTGGATGGTCCT

     CAGAACTTTCCCCAATTACAGGGTGACTCACAGCCGCATTGGTGACTCACTTCAATGTGT
2461 ---------+---------+---------+---------+---------+---------+ 2520
     GTCTTGAAAGGGGTTAATGTCCCACTGAGTGTCGGCGTAACCACTGAGTGAAGTTACACA

     CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGGTGGGTGAGAGAGACA
2521 ---------+---------+---------+---------+---------+---------+ 2580
     GTAAAGGCCGACGACACACACTCGTCACCTGTGCACTCCCCCCCCACCCACTCTCTCTGT

     GGCAGCTCGGATTCAACTACCTTAGATAATATTTCTGAAAACCTACCAGCCAGAGGGTAG
2581 ---------+---------+---------+---------+---------+---------+ 2640
     CCGTCGAGCCTAAGTTGATGGAATCTATTATAAAGACTTTTGGATGGTCGGTCTCCCATC

     GGCACAAAGATGGATGTAATGCACTTTGGGAGGCCAAGGCGGGAGGATTGCTTGAGCCCA
2641 ---------+---------+---------+---------+---------+---------+ 2700
     CCGTGTTTCTACCTACATTACGTGAAACCCTCCGGTTCCGCCCTCCTAACGAACTCGGGT

     GGAGTTCAAGACCAGCCTGGGCAACATACCAAGACCCCCGTCTCTTTAAAAATATATATA
2701 ---------+---------+---------+---------+---------+---------+ 2760
     CCTCAAGTTCTGGTCGGACCCGTTGTATGGTTCTGGGGGCAGAGAAATTTTTATATATAT

     TTTTAAATATACTTAAATATATATTTCTAATATCTTTAAATATATATATATATTTTAAAG
2761 ---------+---------+---------+---------+---------+---------+ 2820
     AAAATTTATATGAATTTATATATAAAGATTATAGAAATTTATATATATATATAAAATTTC

     ACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAATAGAAGC
2821 ---------+---------+---------+---------+---------+------ 2876
     TGGTTAAATACCCTCTTAACGTGTGTCTACACTTTACTTACATTAGATTATCTTCG
```

Fig. 3 (sheet 4/4)

Amino Acid Sequence of Human Plasminogen Activator Inhibitor-1

SEQ ID NO:2

(including Signal Peptide, shown in *italics*)

MQMSPALTCLVLGLALVFGEGSA
Signal peptide

```
   10        20        30        40        50        60
    |         |         |         |         |         |
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQA

   70        80        90       100       110       120
    |         |         |         |         |         |
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST

  130       140       150       160       170       180
    |         |         |         |         |         |
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP

  190       200       210       220       230       240
    |         |         |         |         |         |
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP

  250       260       270       280       290       300
    |         |         |         |         |         |
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR

  310       320       330       340       350       360
    |         |         |         |         |         |
QFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF
                                 *************|**|******
                                              P4 P1
  370
    |
VVRHNPTGTVLFMGQVMEP
```

The Reactive Center Loop (RCL) region is marked by asterisks.

P1 (346) and P4 (343), the preferred sites for substitution, are noted and highlighted.

(Also highlighted are four additional sites which can be substituted to yield a more stable protein: Asn150, Lys154, Gln319, and Met354, Val343)

Figure 4A

Mature human plasminogen activator inhibitor-1 (PAI-1)

SEQ ID NO:3

```
         10        20        30        40        50        60
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQA
         70        80        90       100       110       120
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST
        130       140       150       160       170       180
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP
        190       200       210       220       230       240
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP
        250       260       270       280       290       300
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR
        310       320       330       340       350       360
QFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF
        370
VVRHNPTGTVLFMGQVMEP
```

FIG. 4B

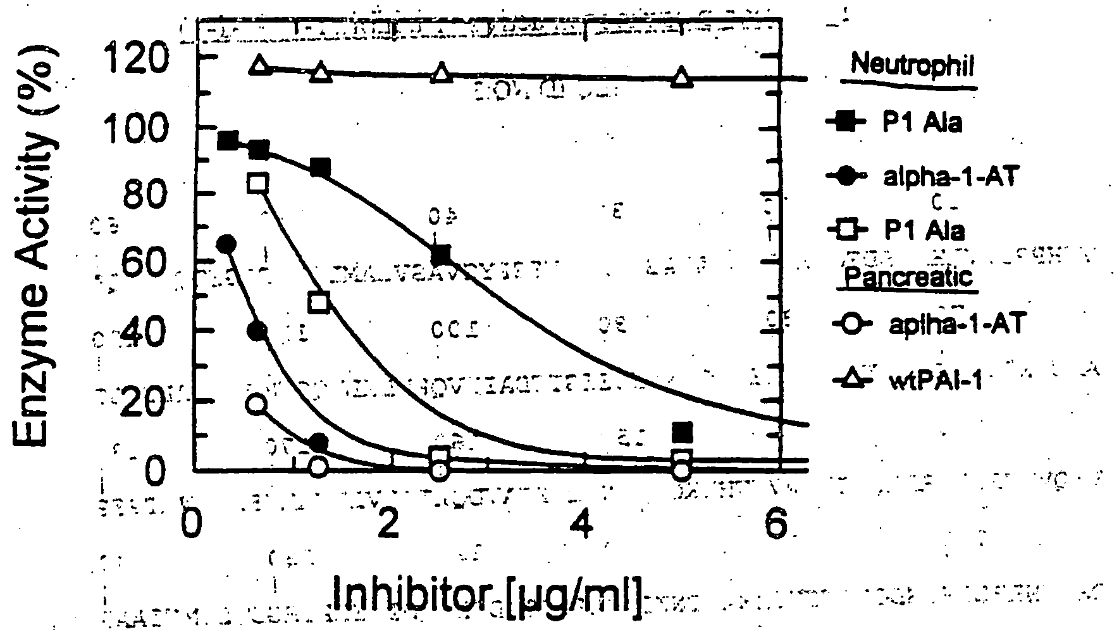

Enzyme Activity (%)
120
100
80
60
40
20
0
0
2
4
6
Inhibitor [µg/ml]
Neutrophil
P1 Ala
alpha-1-AT
P1 Ala
Pancreatic
apiha-1-AT
wtPAI-1

Fig.5

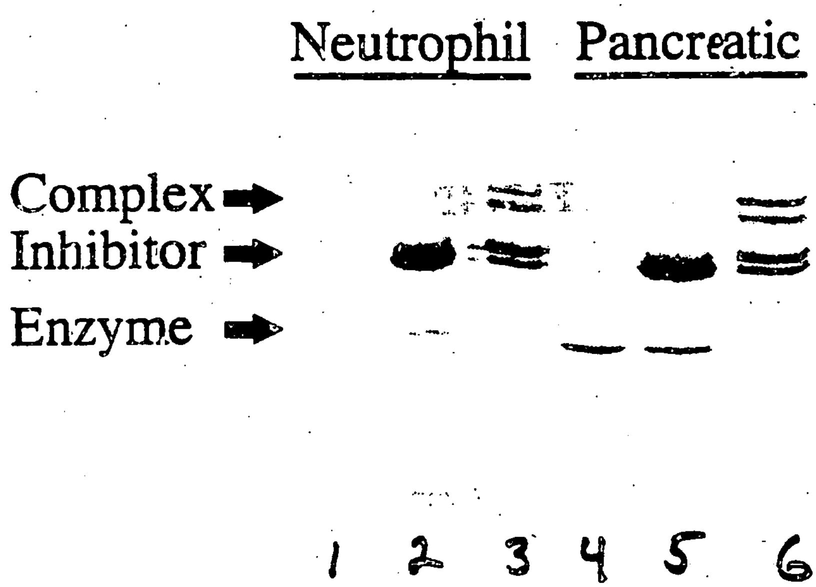
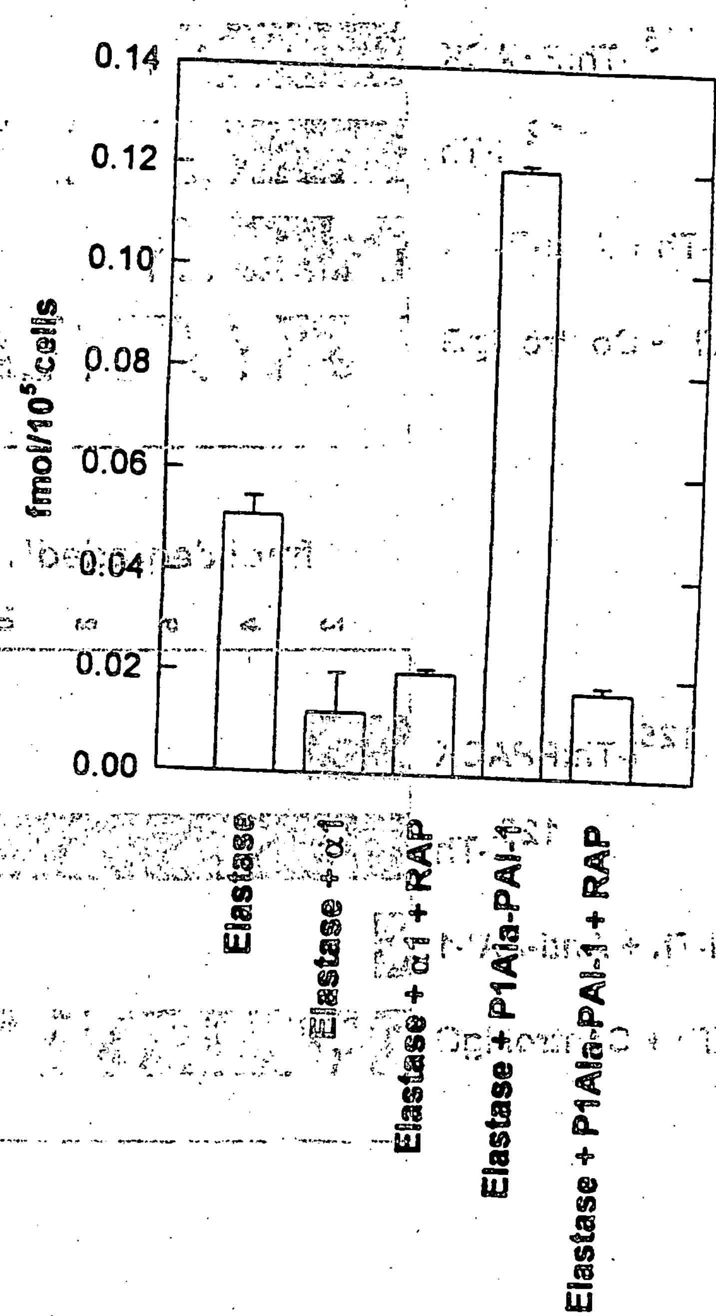

Neutrophil
Pancreatic
Complex
Inhibitor
Enzyme
1 2 3 4 5 6

Fig. 6

Fig. 7


0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
fmol/10^5 cells
Elastase
Elastase + α1
Elastase + α1 + RAP
Elastase + P1Ala-PAI-1
Elastase + P1Ala-PAI-1 + RAP

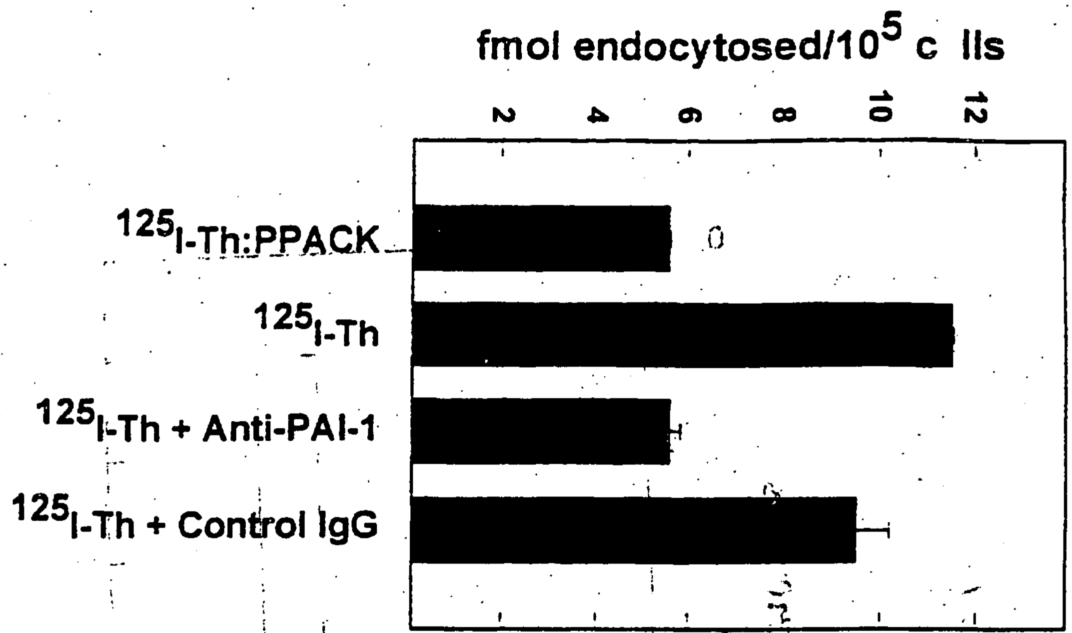

fmol endocytosed/10^5 cells
2
4
6
8
10
12
125I-Th:PPACK
125I-Th
125I-Th + Anti-PAI-1
125I-Th + Control IgG

Fig. 8

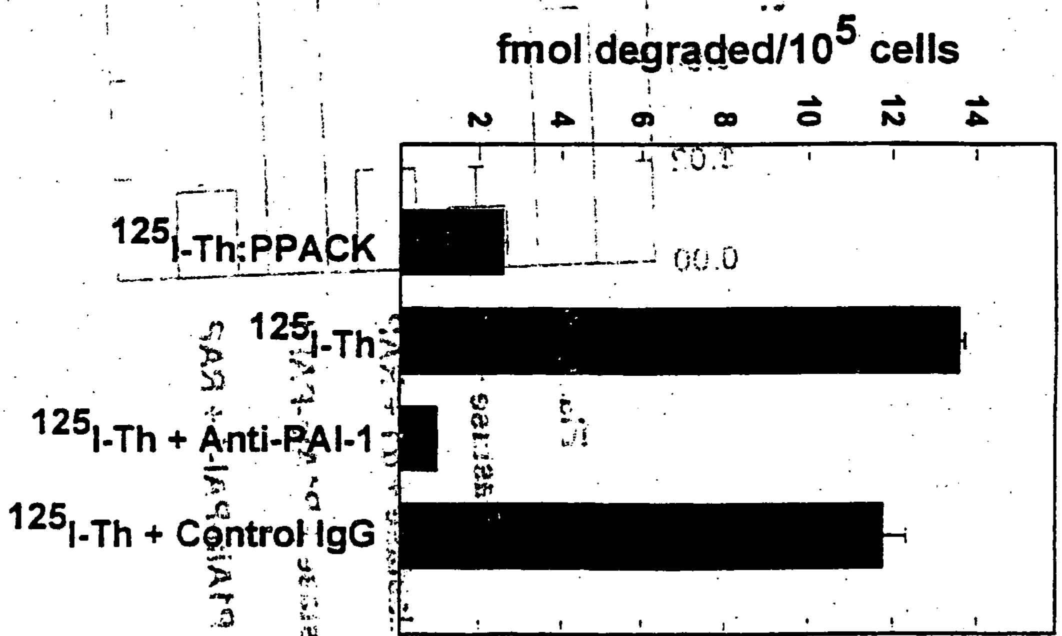

fmol degraded/10^5 cells
2
4
6
8
10
12
14
125I-Th:PPACK
125I-Th
125I-Th + Anti-PAI-1
125I-Th + Control IgG

Fig. 9

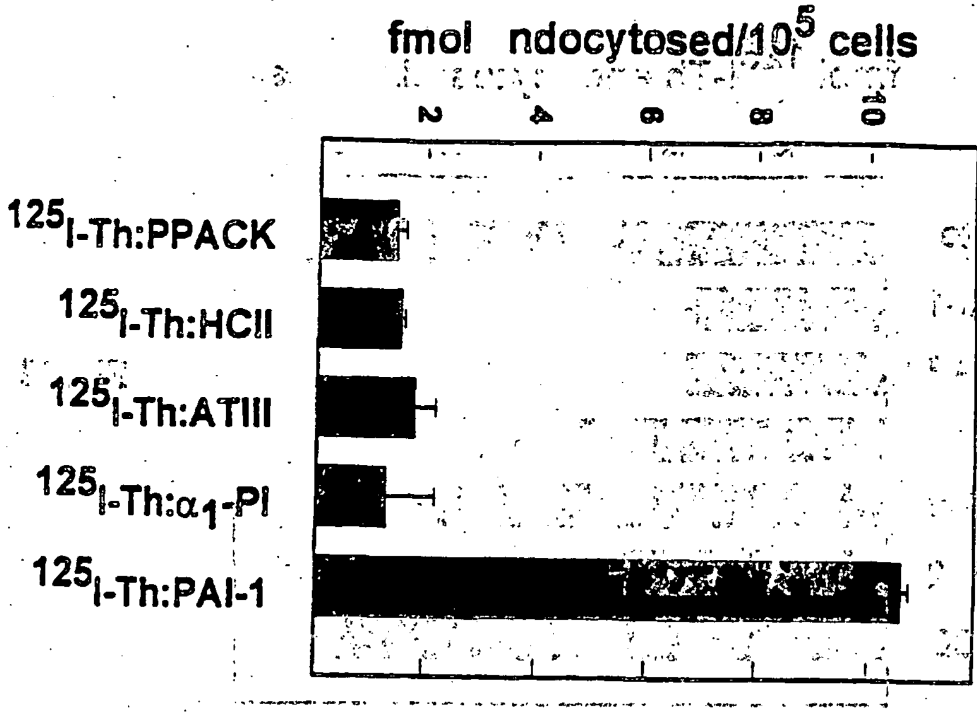

fmol ndocytosed/10^5 cells
2
4
6
8
10
125I-Th:PPACK
125I-Th:HCII
125I-Th:ATIII
125I-Th:α1-PI
125I-Th:PAI-1

Fig. 10

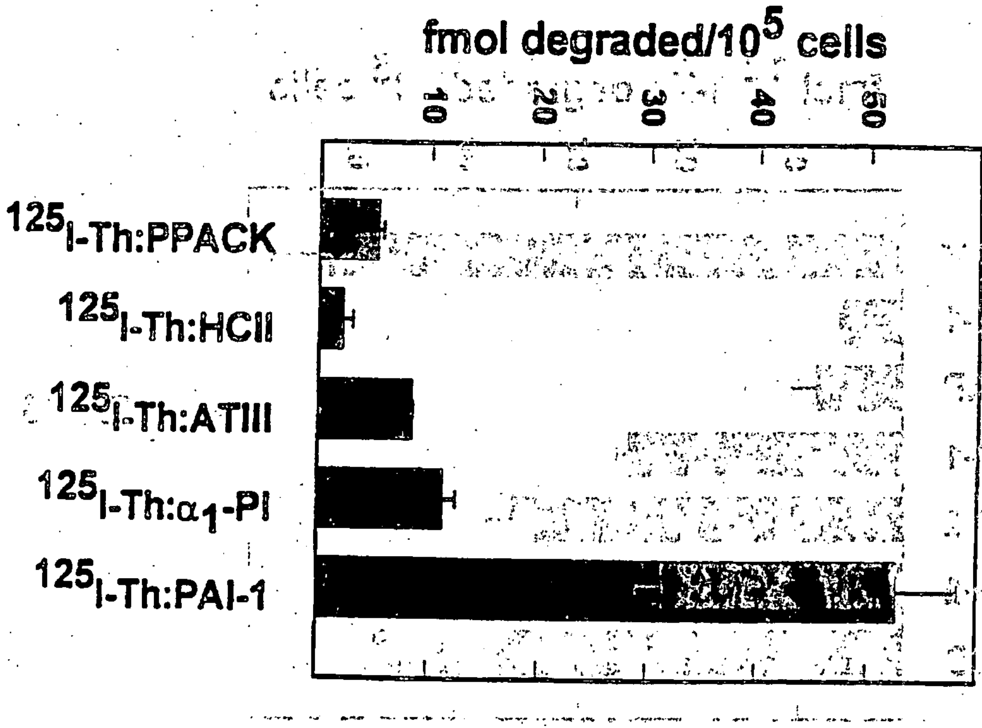

fmol degraded/10^5 cells
10
20
30
40
50
125I-Th:PPACK
125I-Th:HCII
125I-Th:ATIII
125I-Th:α1-PI
125I-Th:PAI-1

Fig. 11

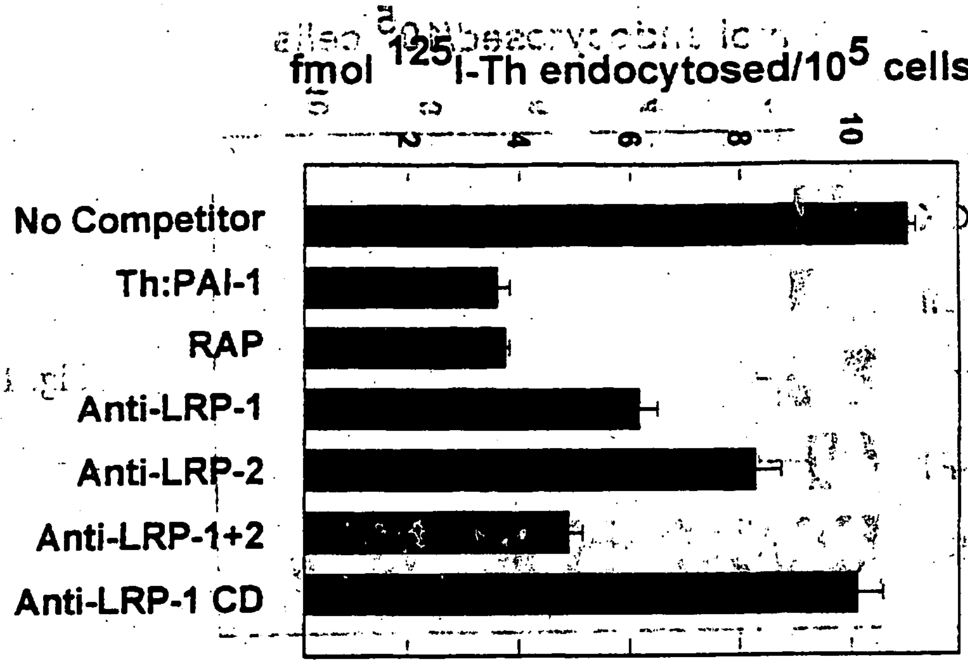

fmol 125I-Th endocytosed/10^5 cells
2
4
6
8
10
No Competitor
Th:PAI-1
RAP
Anti-LRP-1
Anti-LRP-2
Anti-LRP-1+2
Anti-LRP-1 CD

Fig. 12

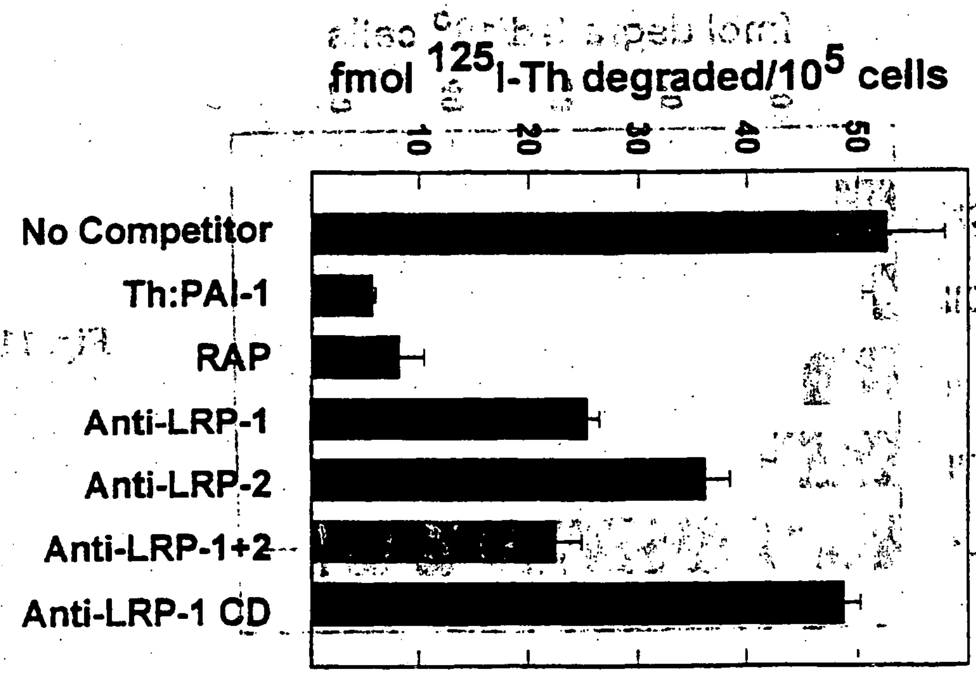

fmol 125I-Th degraded/10^5 cells
10
20
30
40
50
No Competitor
Th:PAI-1
RAP
Anti-LRP-1
Anti-LRP-2
Anti-LRP-1+2
Anti-LRP-1 CD

Fig. 13

Fig. 14

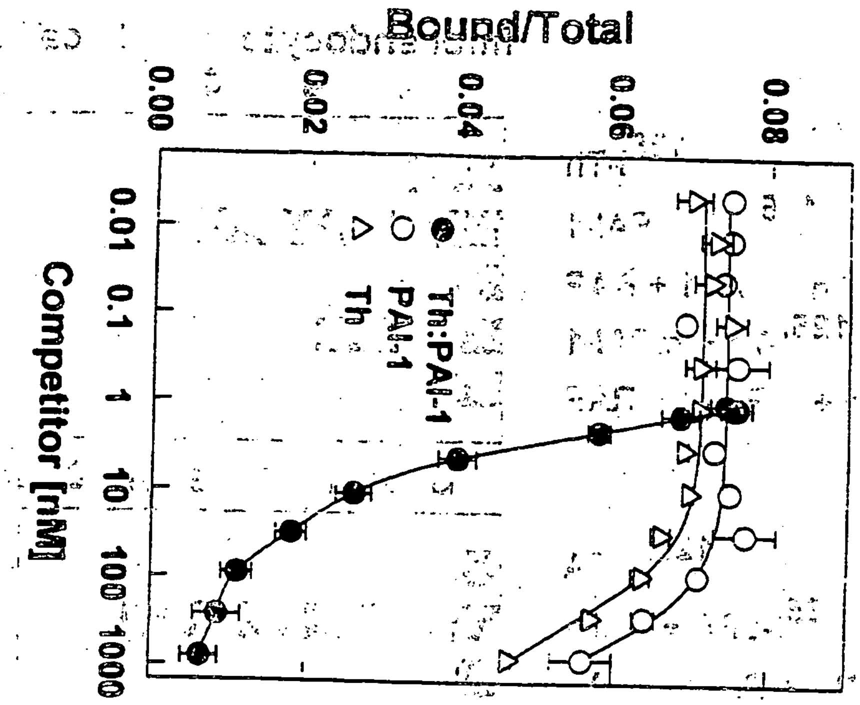
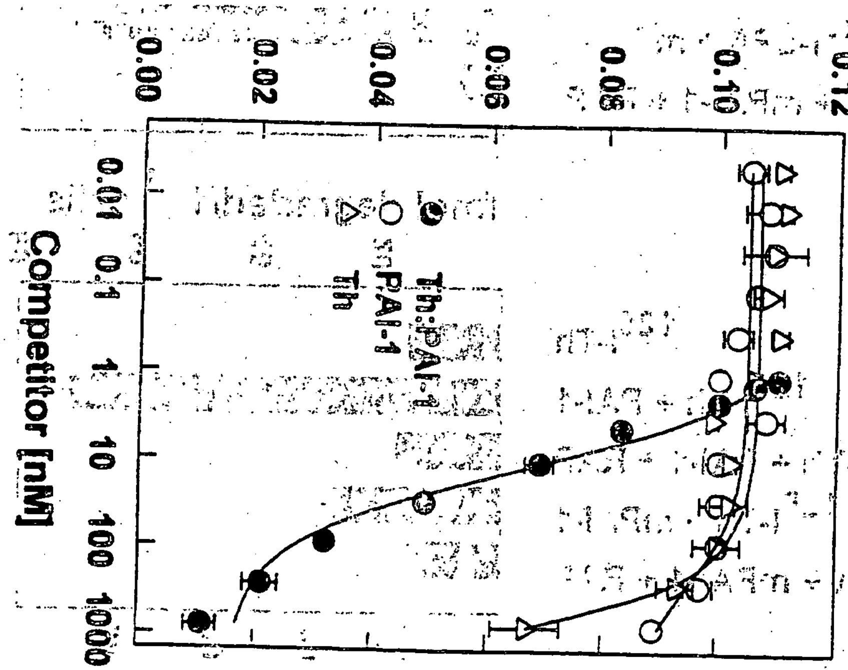

Bound/Total
0.00
0.02
0.04
0.06
0.08
0.01
0.1
1
10
100
1000
Competitor [nM]
Th:PAI-1
PAI-1
Th

Fig. 15


0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.01
0.1
1
10
100
1000
Competitor [nM]
Th:PAI-1
sPAI-1
Th

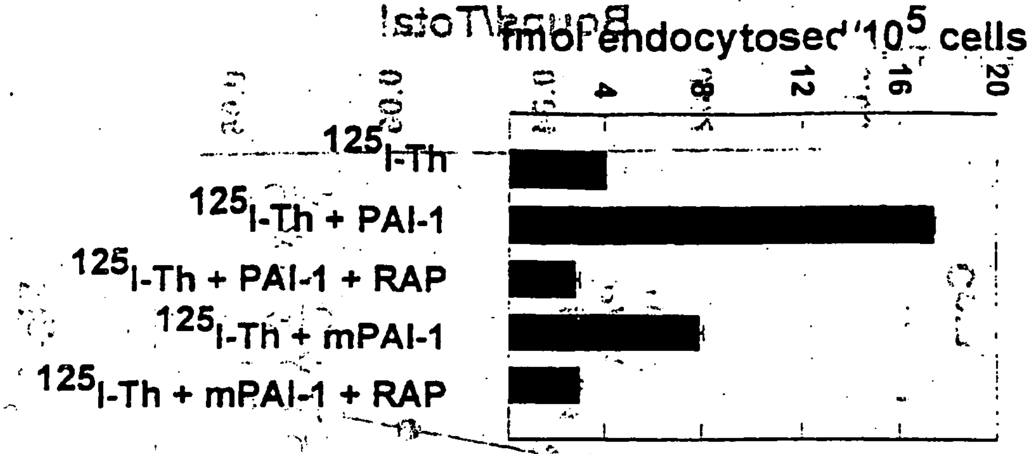


Fig. 16

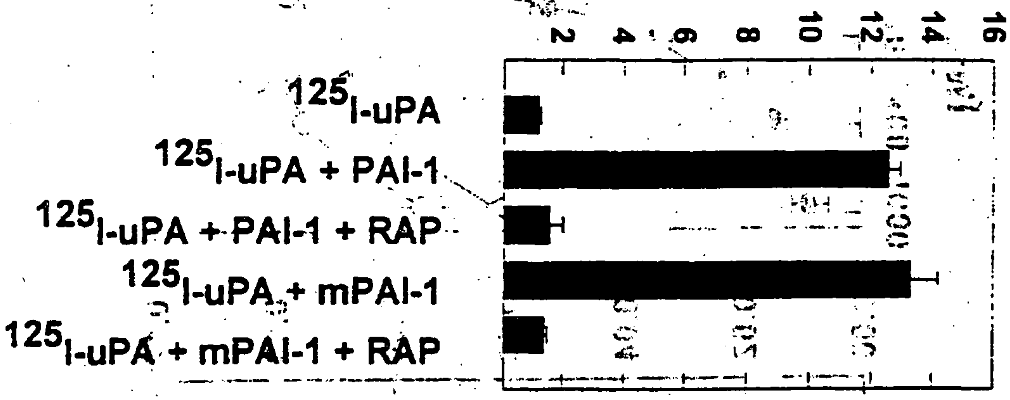


Fig. 17

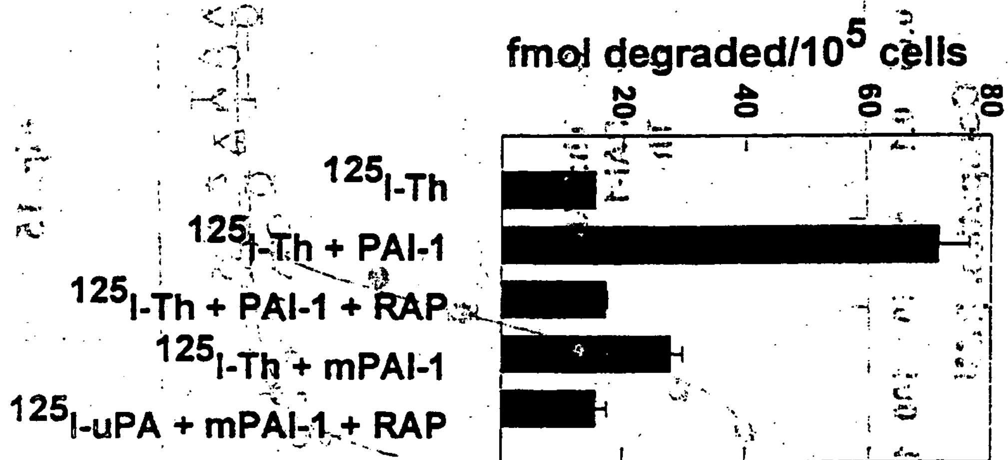


Fig. 18

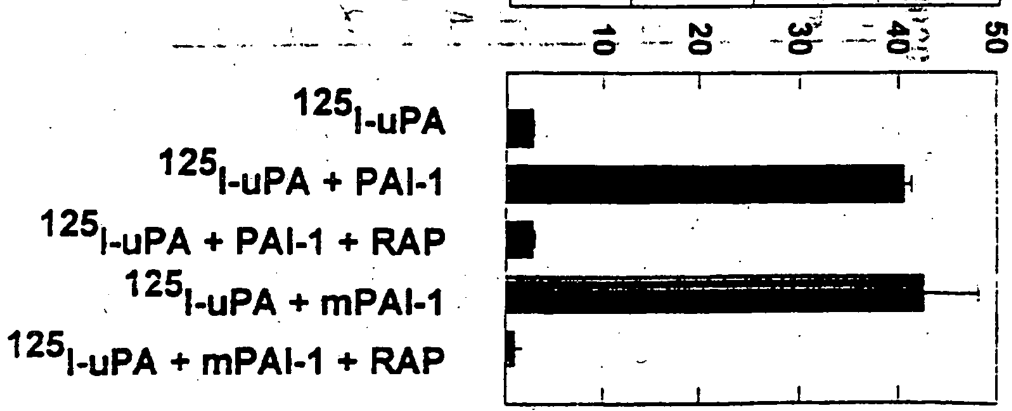


Fig. 19

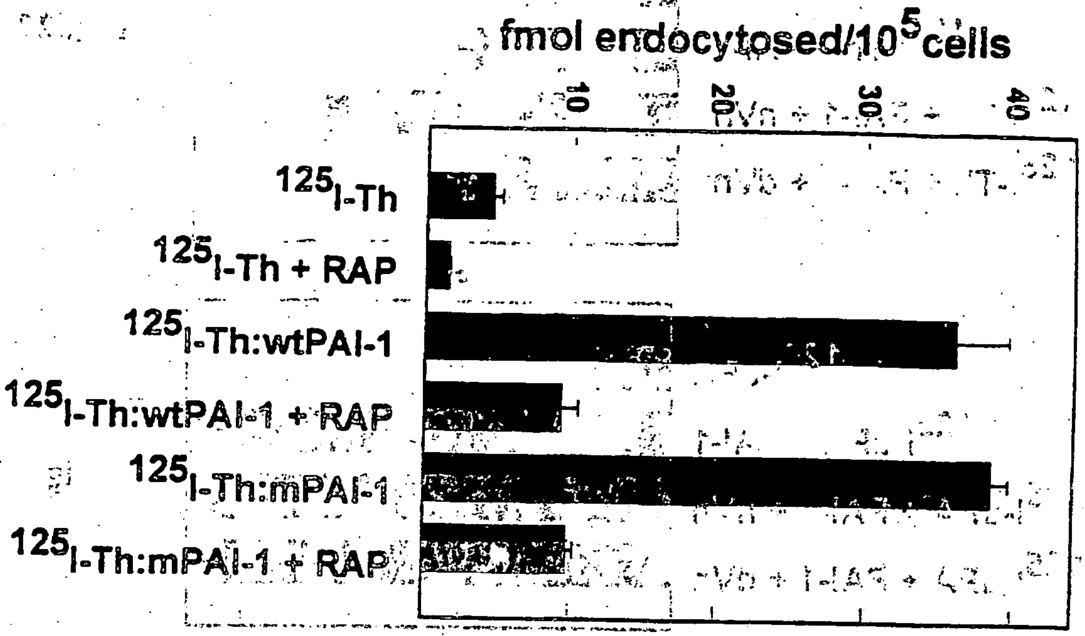

fmol endocytosed/10^5 cells
10
20
30
40
125I-Th
125I-Th + RAP
125I-Th:wtPAI-1
125I-Th:wtPAI-1 + RAP
125I-Th:mPAI-1
125I-Th:mPAI-1 + RAP

Fig. 20

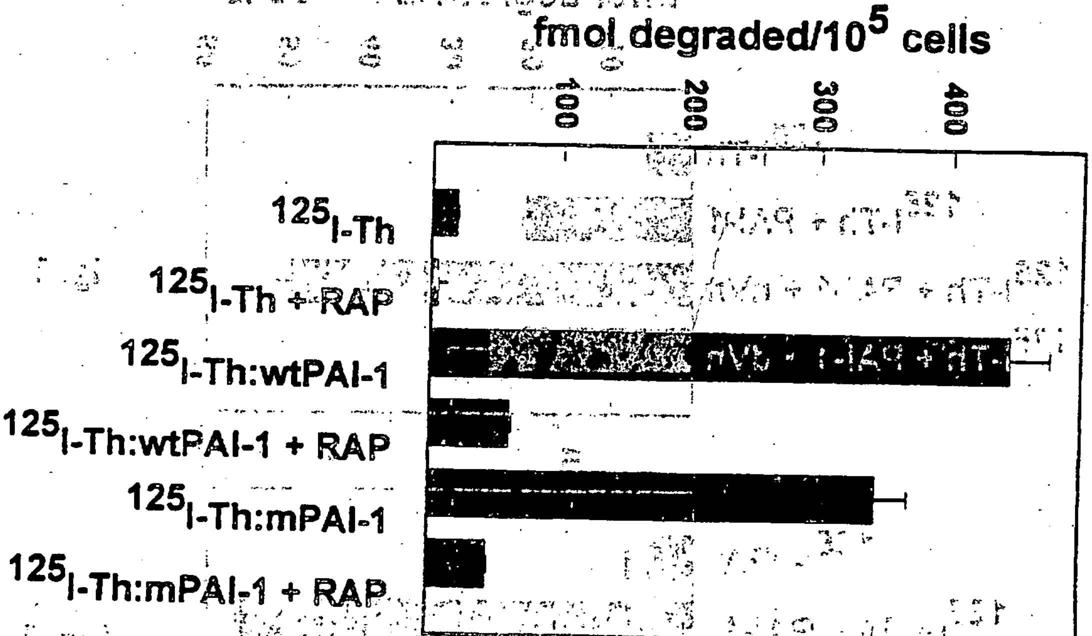

fmol degraded/10^5 cells
100
200
300
400
125I-Th
125I-Th + RAP
125I-Th:wtPAI-1
125I-Th:wtPAI-1 + RAP
125I-Th:mPAI-1
125I-Th:mPAI-1 + RAP

Fig. 21

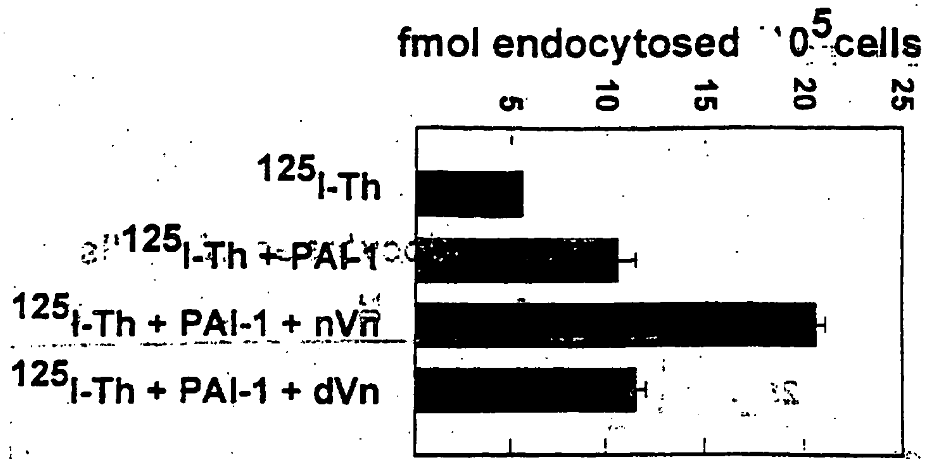


Fig. 22

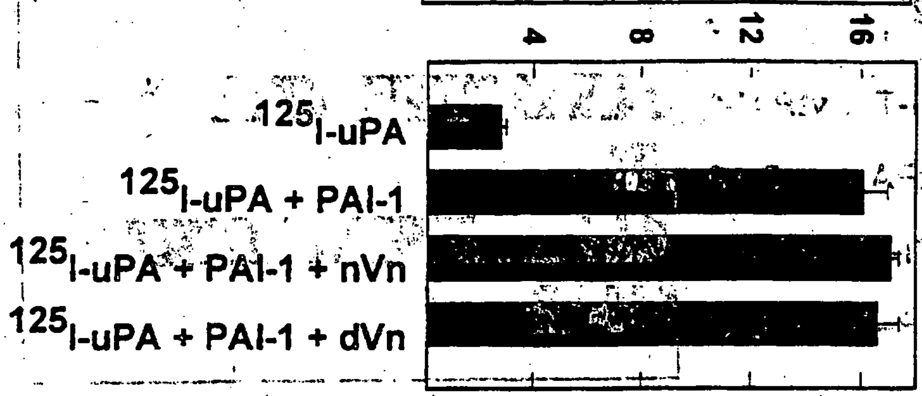


Fig. 23

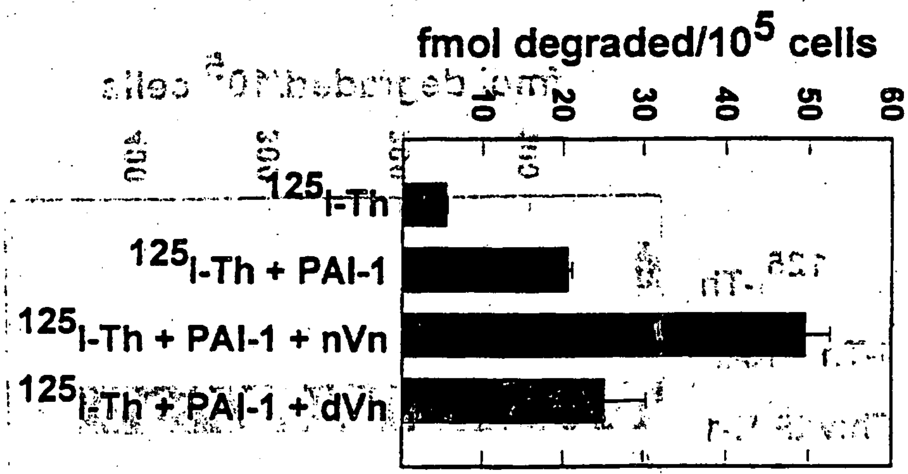


Fig. 24

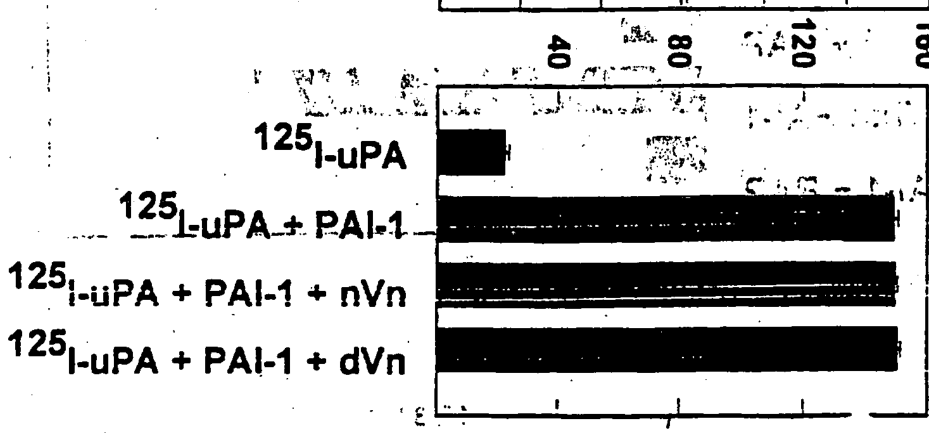


Fig. 25

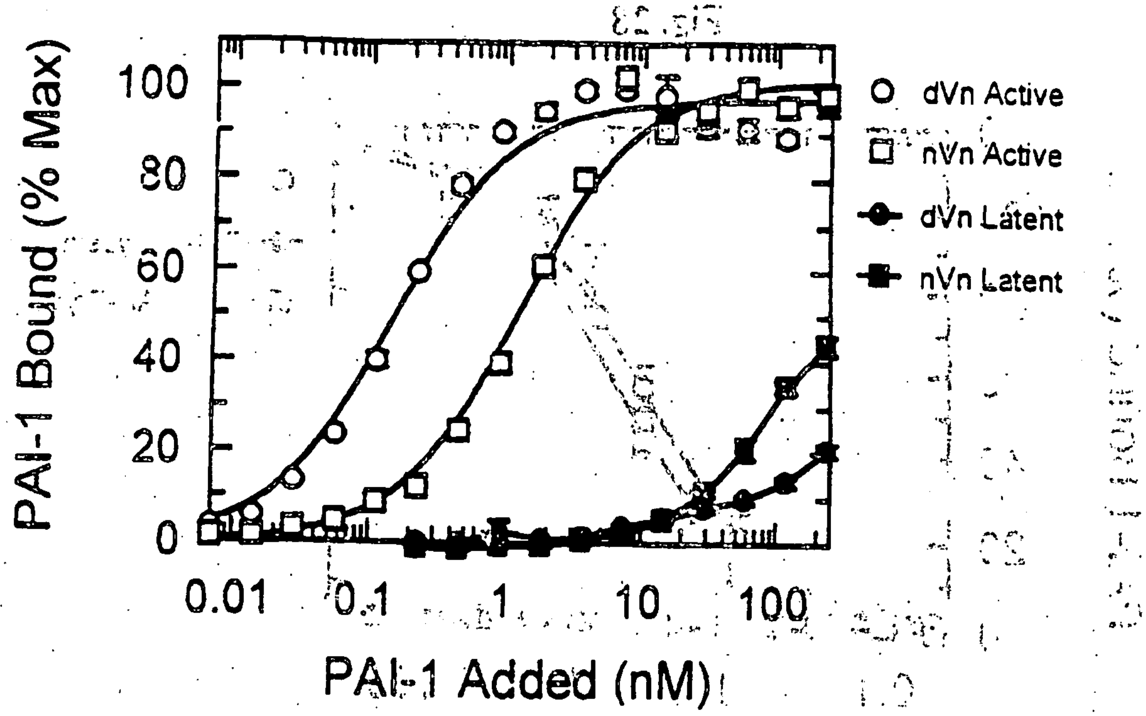

PAI-1 Bound (% Max)
100
80
60
40
20
0
0.01
0.1
1
10
100
PAI-1 Added (nM)
dVn Active
nVn Active
dVn Latent
nVn Latent

Fig. 26

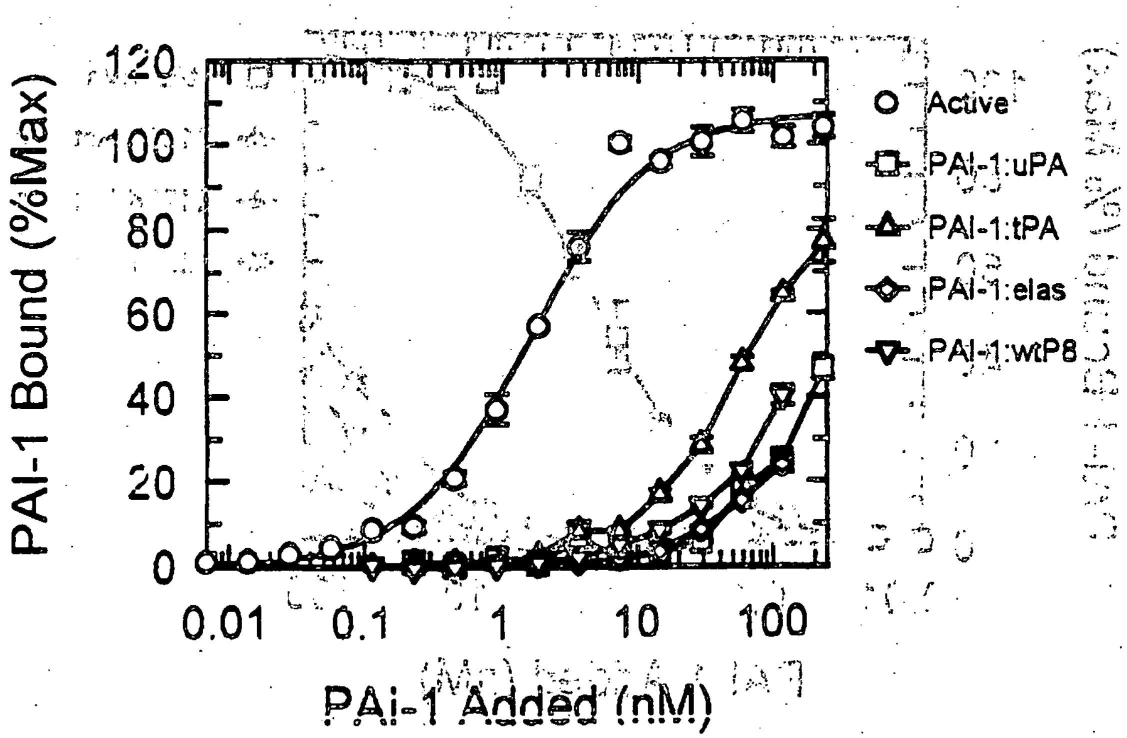
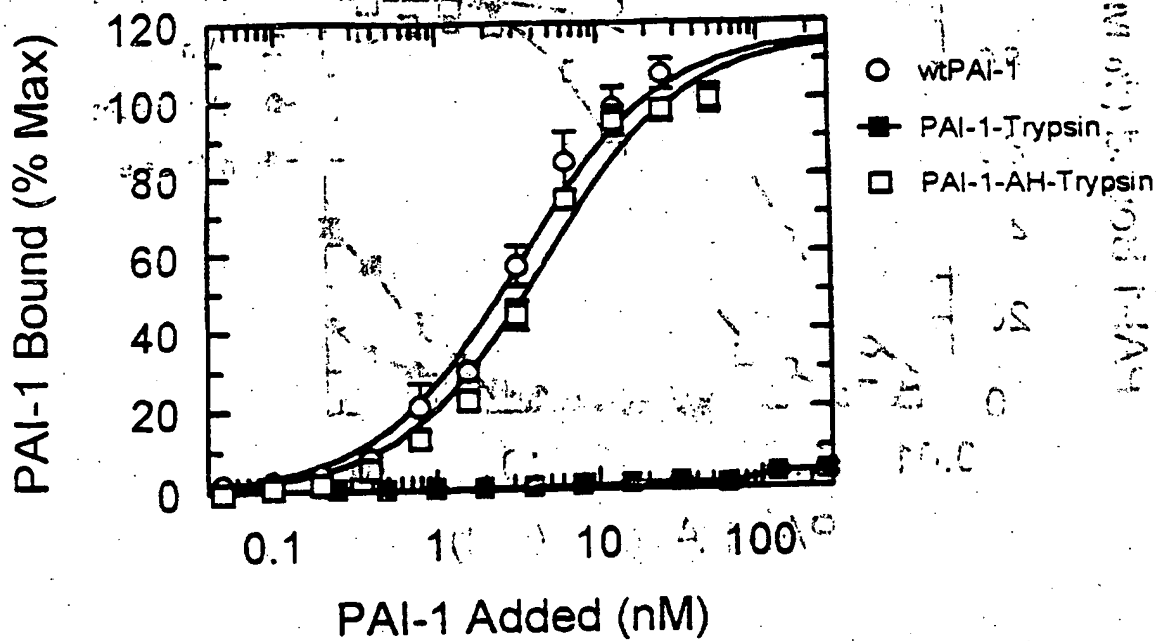

PAI-1 Bound (%Max)
120
100
80
60
40
20
0
0.01
0.1
1
10
100
PAI-1 Added (nM)
Active
PAI-1:uPA
PAI-1:tPA
PAI-1:elas
PAI-1:wtP8

Fig. 27

Fig. 28


PAI-1 Bound (% Max)
0
20
40
60
80
100
120
0.1
1
10
100
PAI-1 Added (nM)
wtPAI-1
PAI-1-Trypsin
PAI-1-AH-Trypsin

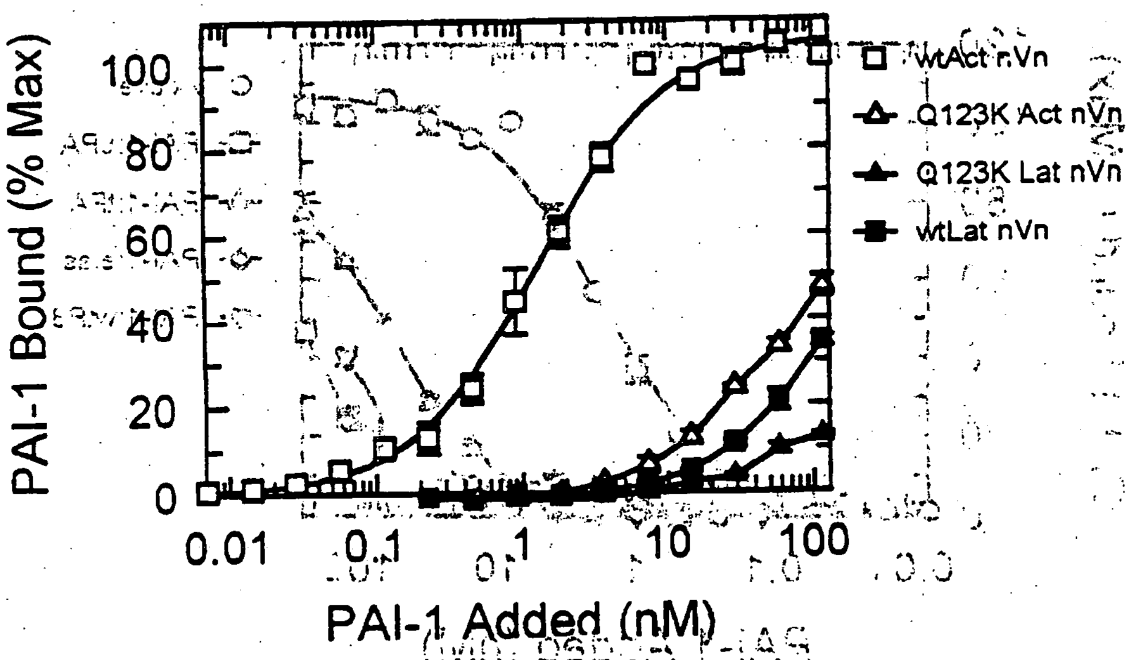

PAI-1 Bound (% Max)
0
20
40
60
80
100
0.01
0.1
1
10
100
PAI-1 Added (nM)
wtAct nVn
Q123K Act nVn
Q123K Lat nVn
wtLat nVn

Fig. 29

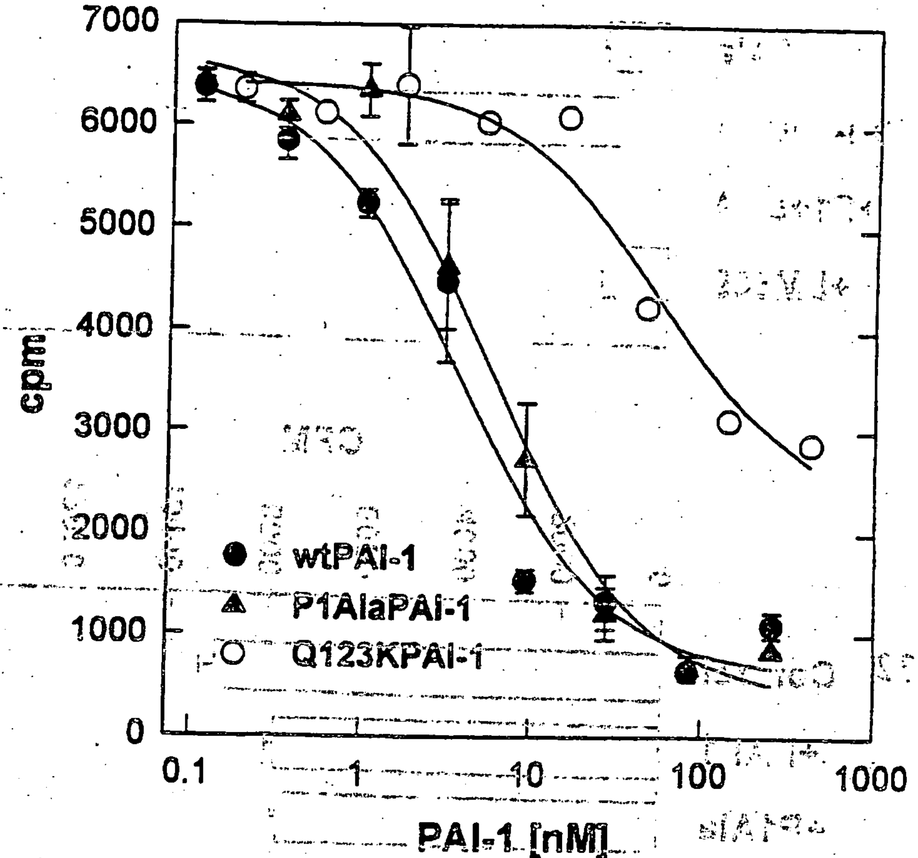

7000
6000
5000
4000
3000
2000
1000
0
cpm
0.1
1
10
100
1000
PAI-1 [nM]
wtPAI-1
P1AlaPAI-1
Q123KPAI-1

Fig. 30

Fig. 31

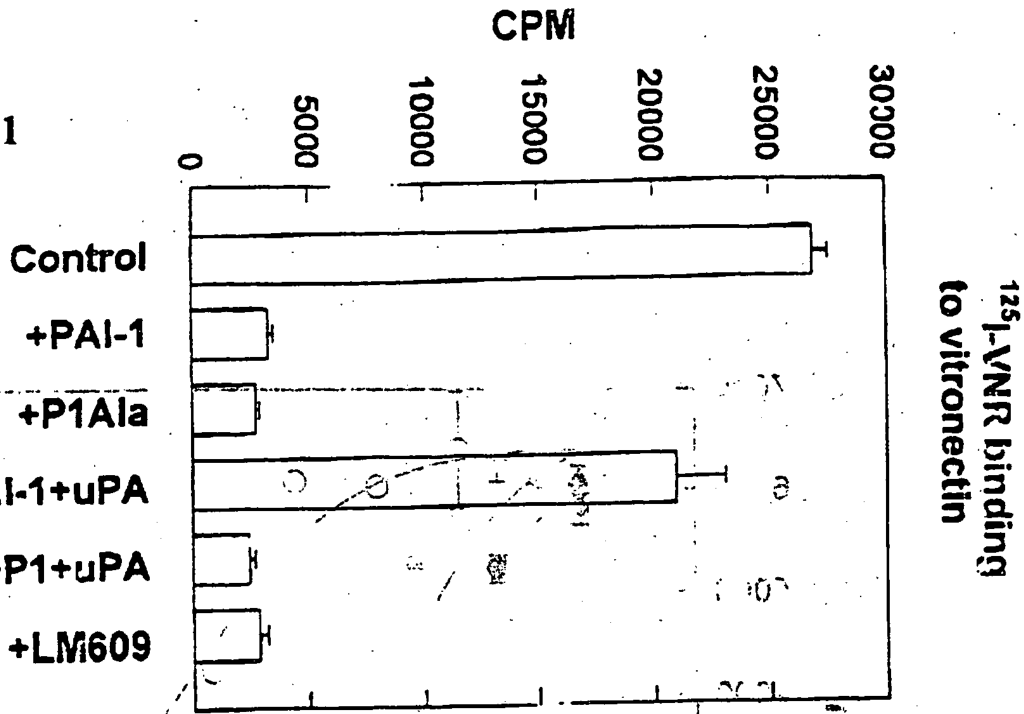

CPM
0
5000
10000
15000
20000
25000
30000
Control
+PAI-1
+P1Ala
+PAI-1+uPA
+P1+uPA
+LM609
^{125}I-VNR binding to vitronectin

Fig. 32

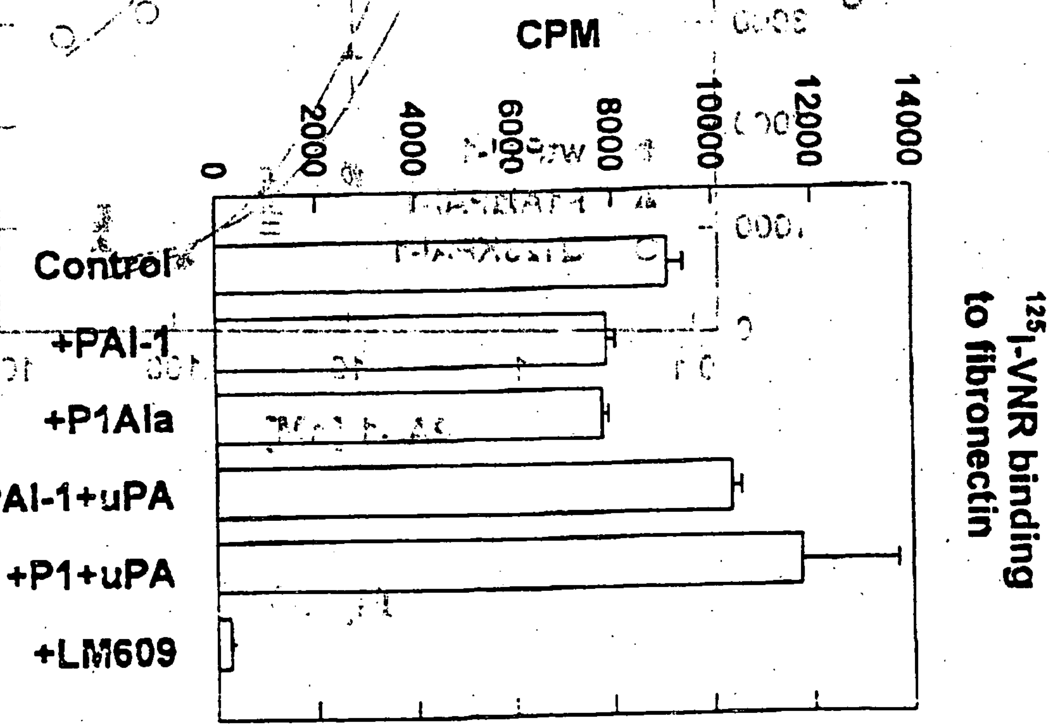

CPM
0
2000
4000
6000
8000
10000
12000
14000
Control
+PAI-1
+P1Ala
+PAI-1+uPA
+P1+uPA
+LM609
^{125}I-VNR binding to fibronectin

Fig. 33

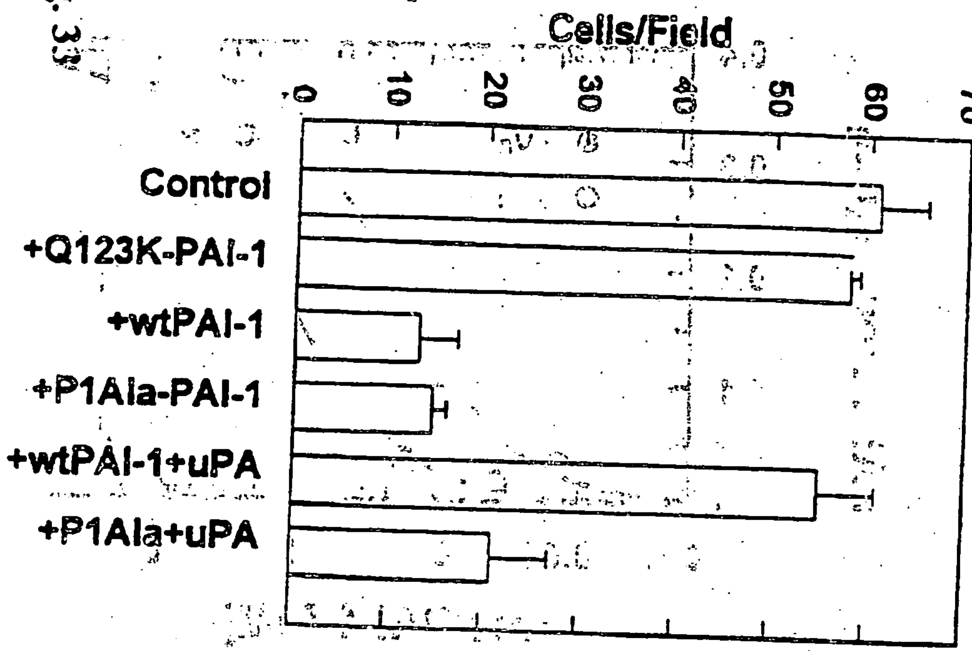

Cells/Field
0
10
20
30
40
50
60
70
Control
+Q123K-PAI-1
+wtPAI-1
+P1Ala-PAI-1
+wtPAI-1+uPA
+P1Ala+uPA

Fig. 34

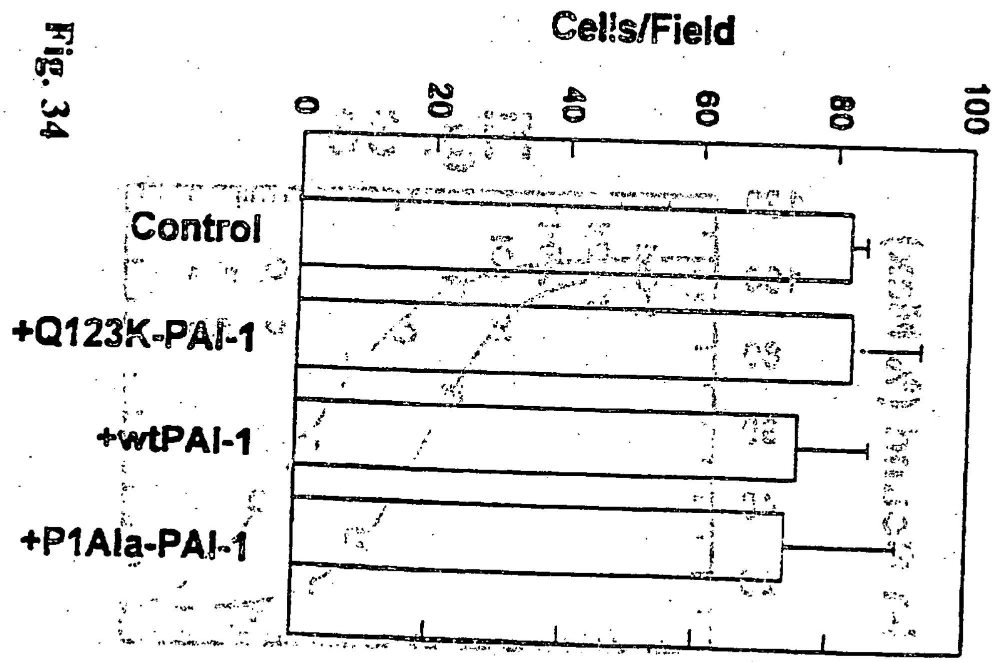
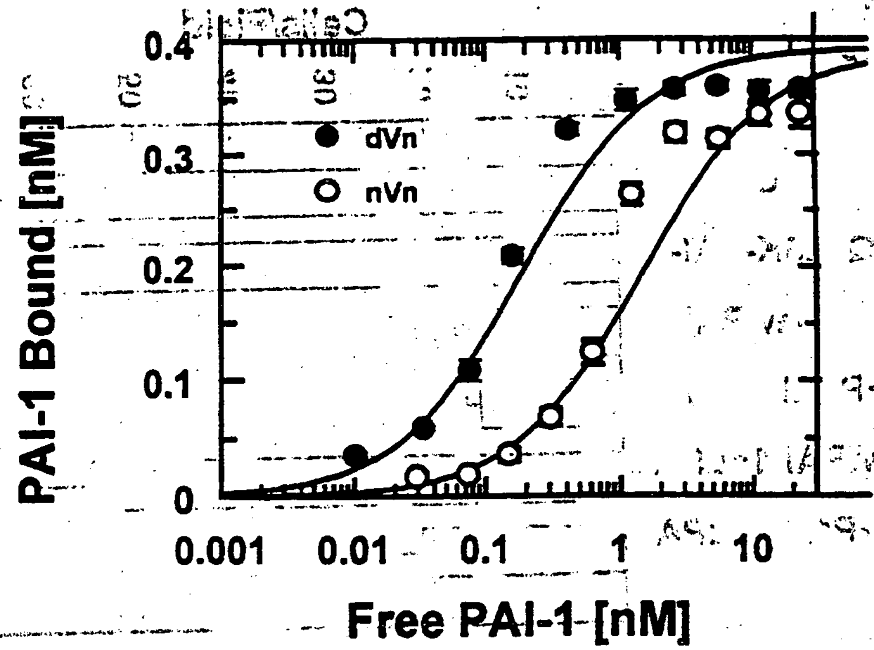
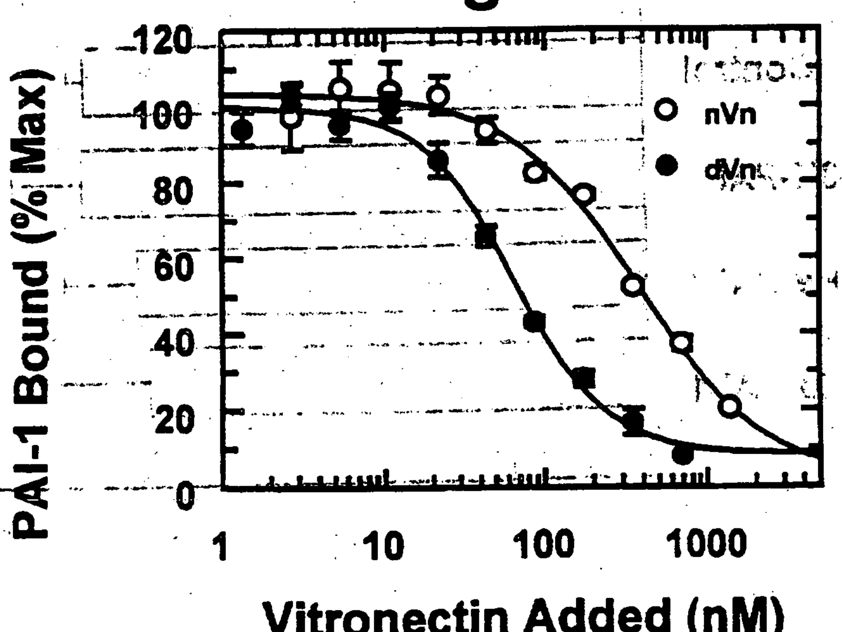

Cells/Field
0
20
40
60
80
100
Control
+Q123K-PAI-1
+wtPAI-1
+P1Ala-PAI-1

Fig. 35



PAI-1 Bound [nM]
0.4
0.3
0.2
0.1
0
dVn
nVn
0.001
0.01
0.1
1
10
Free PAI-1 [nM]

Fig. 36



PAI-1 Bound (% Max)
120
100
80
60
40
20
0
nVn
dVn
1
10
100
1000
Vitronectin Added (nM)

Fig. 37

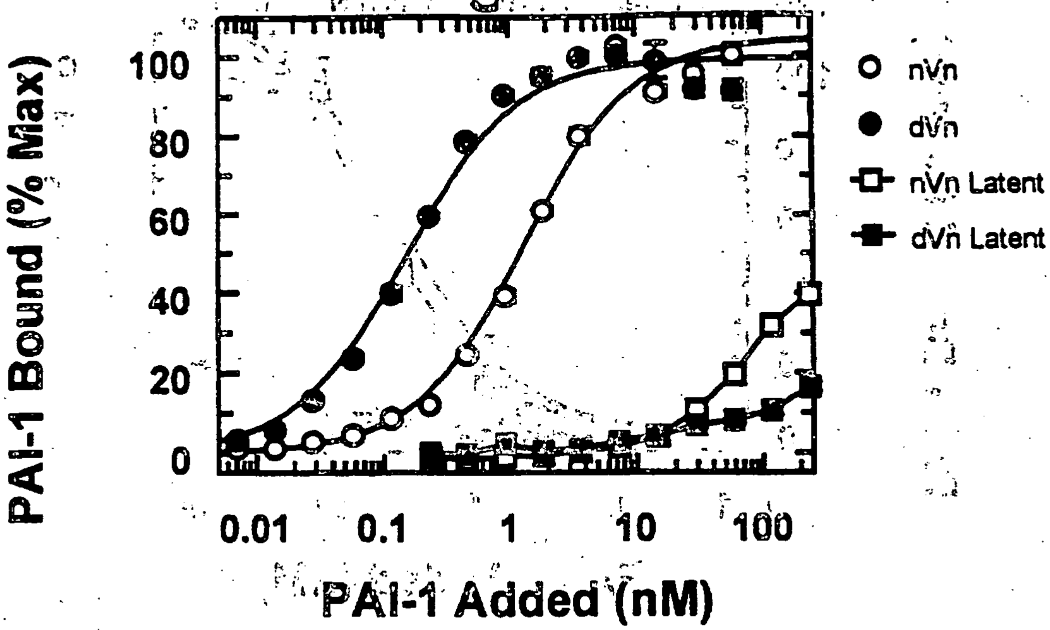

100
80
60
40
20
0
PAI-1 Bound (% Max)
0.01
0.1
1
10
100
PAI-1 Added (nM)
nVn
dVn
nVn Latent
dVn Latent

Fig. 38

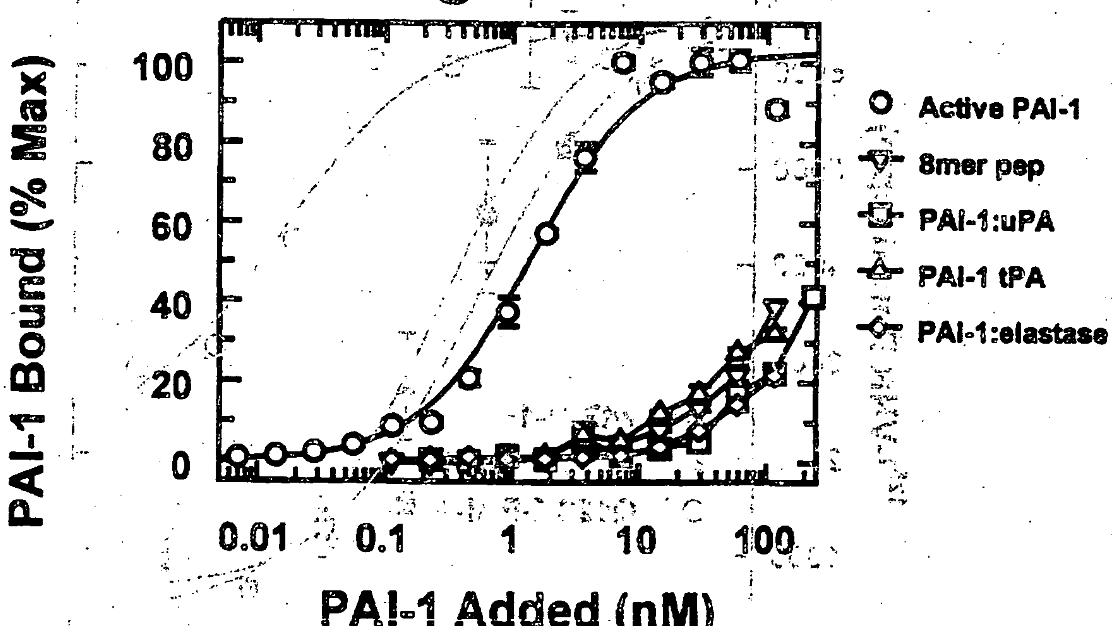

100
80
60
40
20
0
PAI-1 Bound (% Max)
0.01
0.1
1
10
100
PAI-1 Added (nM)
Active PAI-1
8mer pep
PAI-1:uPA
PAI-1 tPA
PAI-1:elastase

Fig. 39

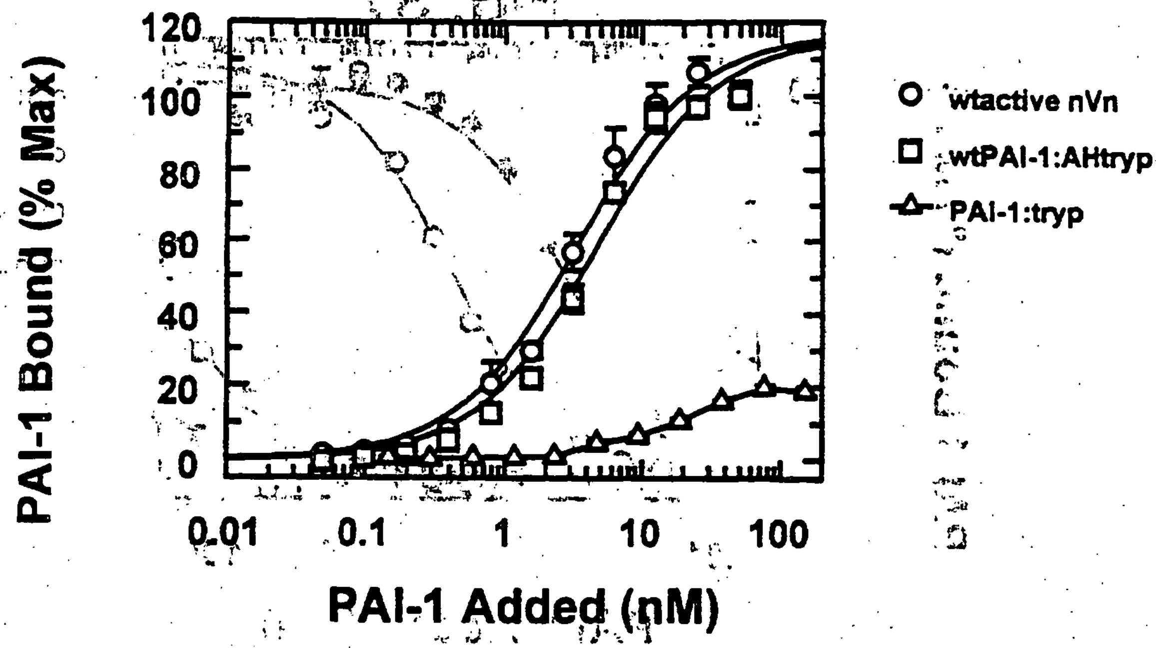
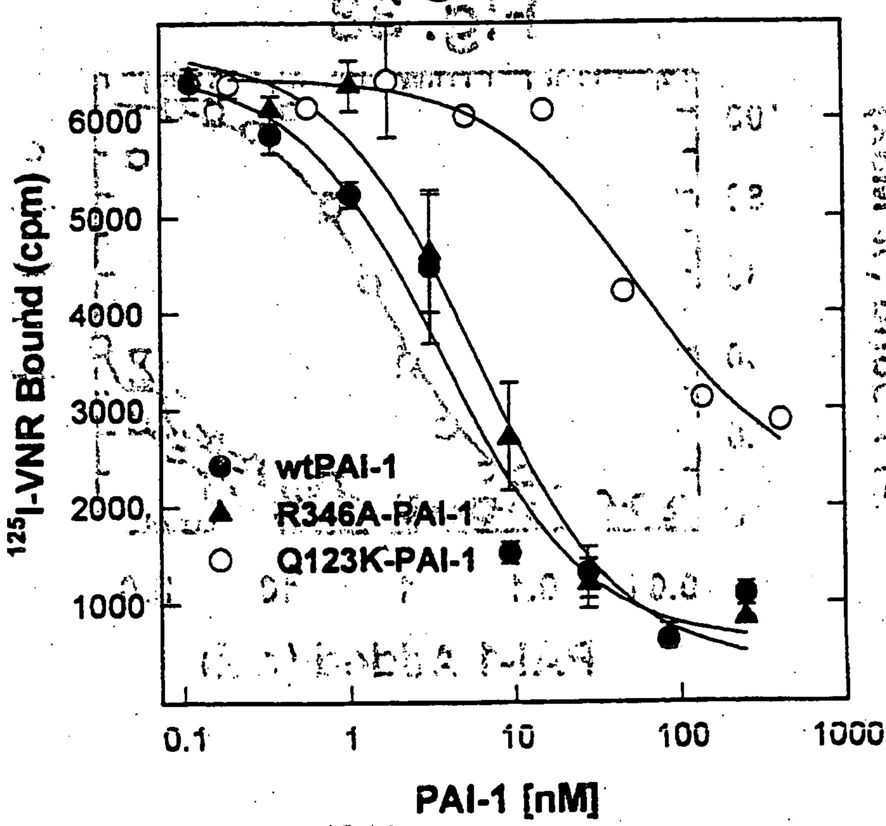
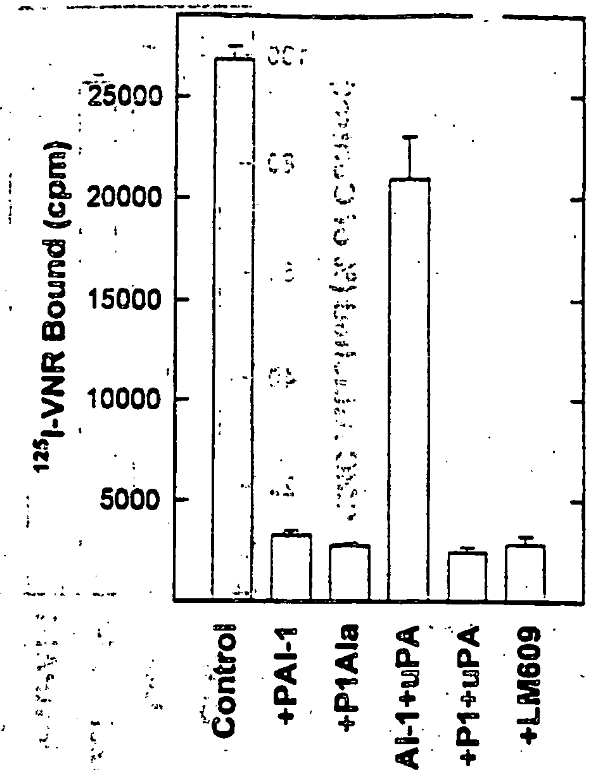

PAI-1 Bound (% Max)
120
100
80
60
40
20
0
0.01
0.1
1
10
100
PAI-1 Added (nM)
wtactive nVn
wtPAI-1:AHtryp
PAI-1:tryp

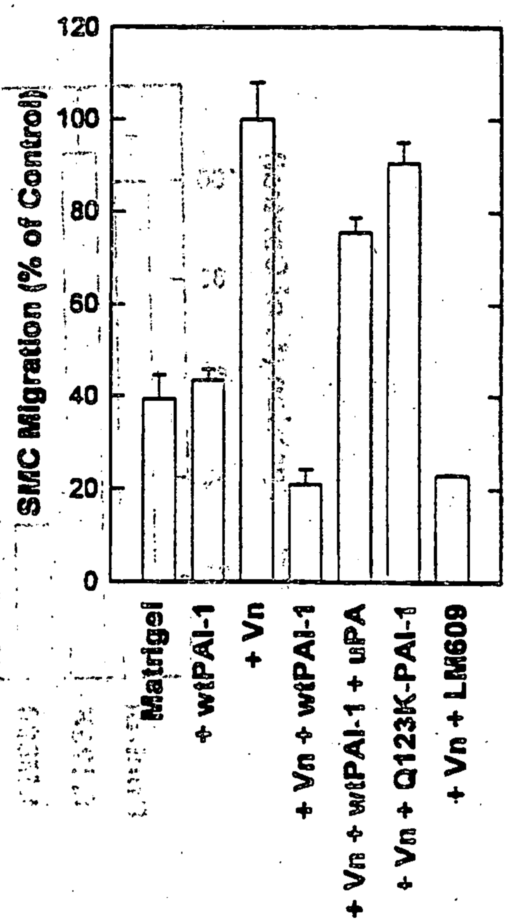
Fig. 40


125I-VNR Bound (cpm)
6000
5000
4000
3000
2000
1000
0.1
1
10
100
1000
PAI-1 [nM]
wtPAI-1
R346A-PAI-1
Q123K-PAI-1



125I-VNR Bound (cpm)
25000
20000
15000
10000
5000
Control
+PAI-1
+P1Ala
+PAI-1+uPA
+P1+uPA
+LM609

Fig. 41



SMC Migration (% of Control)
120
100
80
60
40
20
0
Matrigel
+ wtPAI-1
+ Vn
+ Vn + wtPAI-1
+ Vn + wtPAI-1 + uPA
+ Vn + Q123K-PAI-1
+ Vn + LM609

Fig. 43

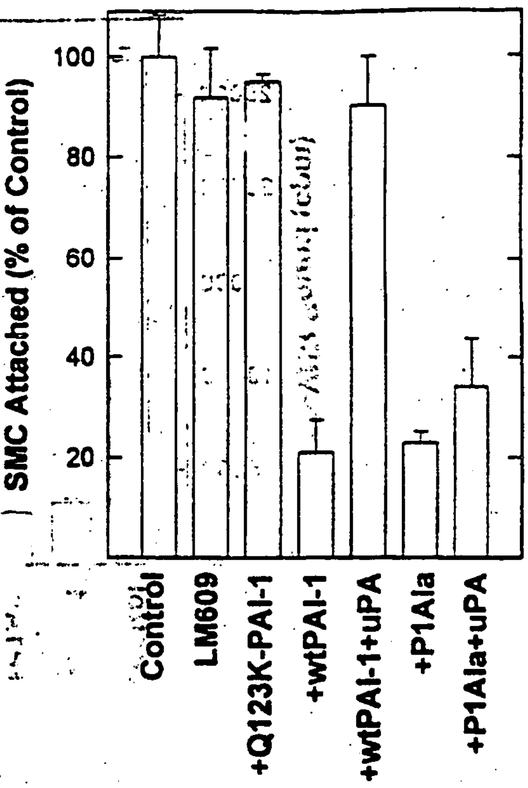


Fig. 42A

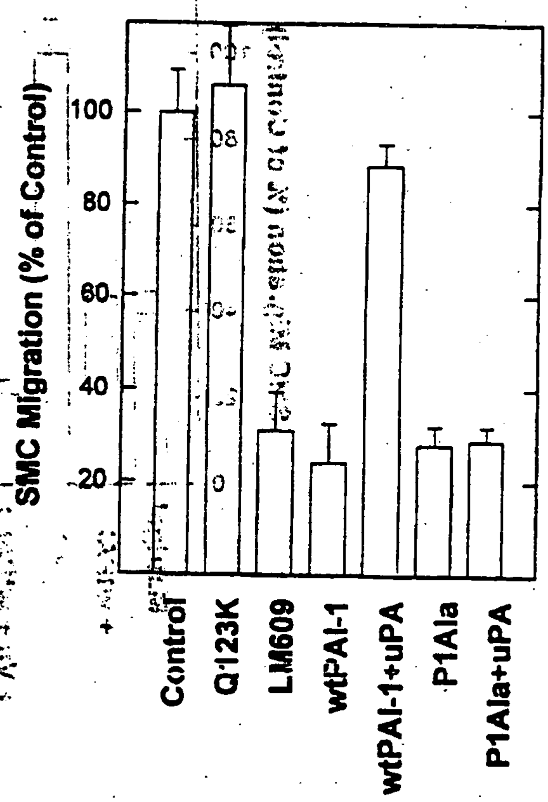


Fig. 42B

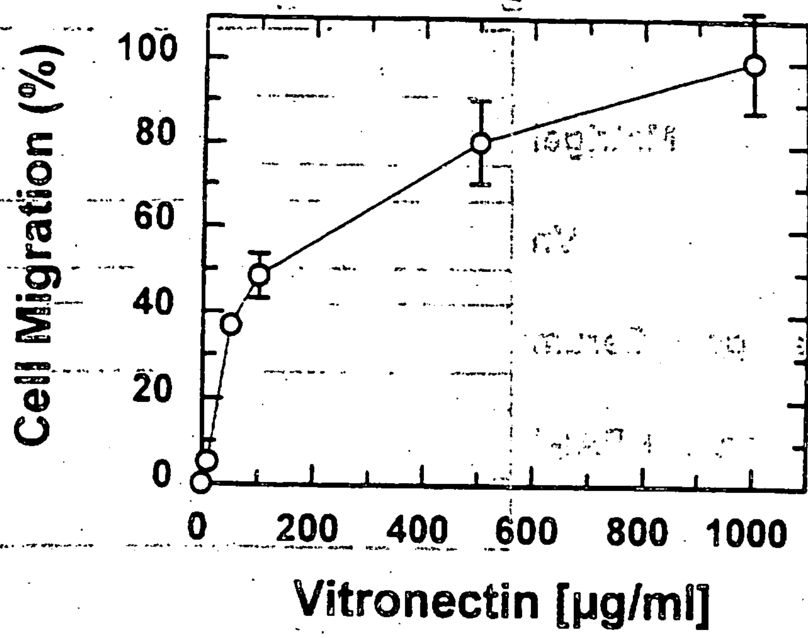

Cell Migration (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Vitronectin [µg/ml]

Fig. 44

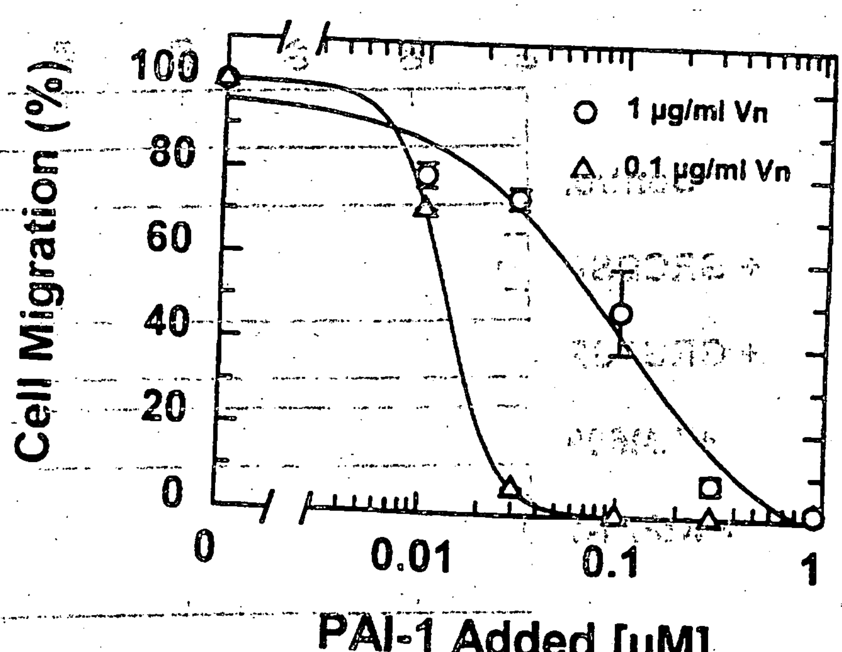
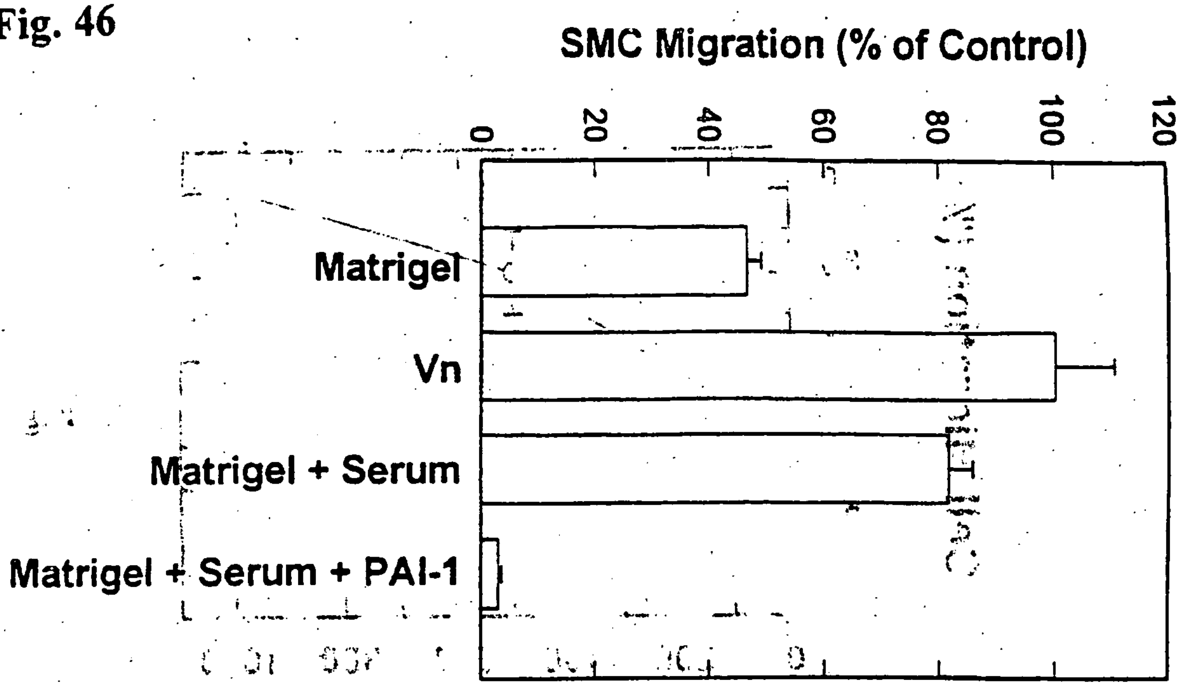

Cell Migration (%)
100
80
60
40
20
0
1 µg/ml Vn
0.1 µg/ml Vn
0
0.01
0.1
1
PAI-1 Added [µM]

Fig. 45

Fig. 46


SMC Migration (% of Control)
0
20
40
60
80
100
120
Matrigel
Vn
Matrigel + Serum
Matrigel + Serum + PAI-1

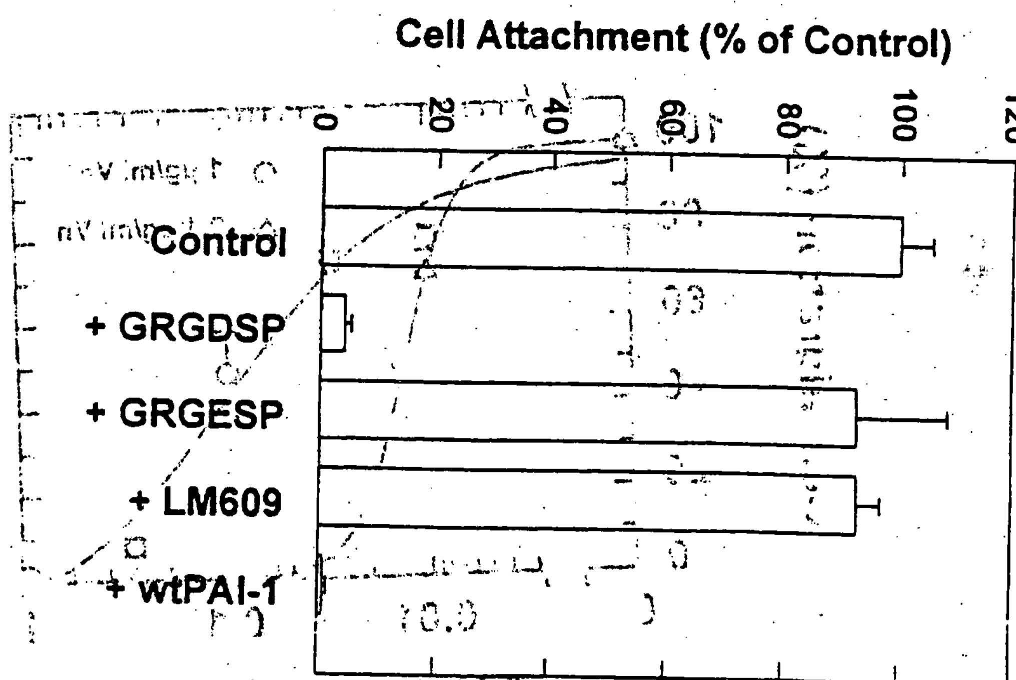

Cell Attachment (% of Control)
0
20
40
60
80
100
120
Control
+ GRGDSP
+ GRGESP
+ LM609
+ wtPAI-1

Fig. 47

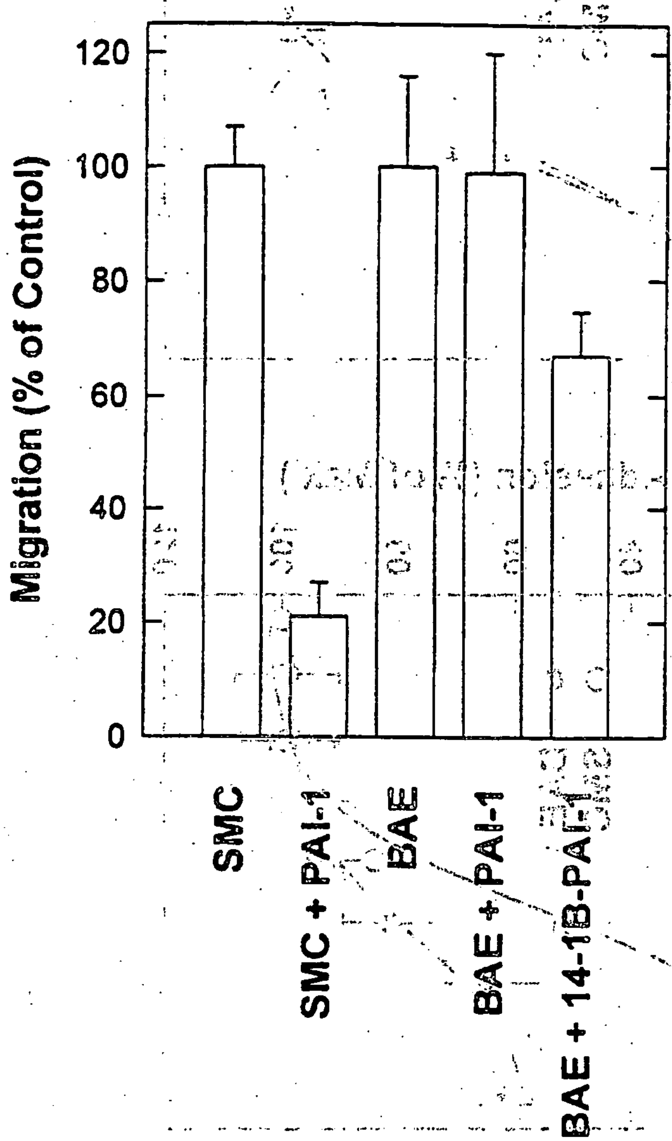

Migration (% of Control)
120
100
80
60
40
20
0
SMC
SMC + PAI-1
BAE
BAE + PAI-1
BAE + 14-1B-PAI-1

Fig. 48

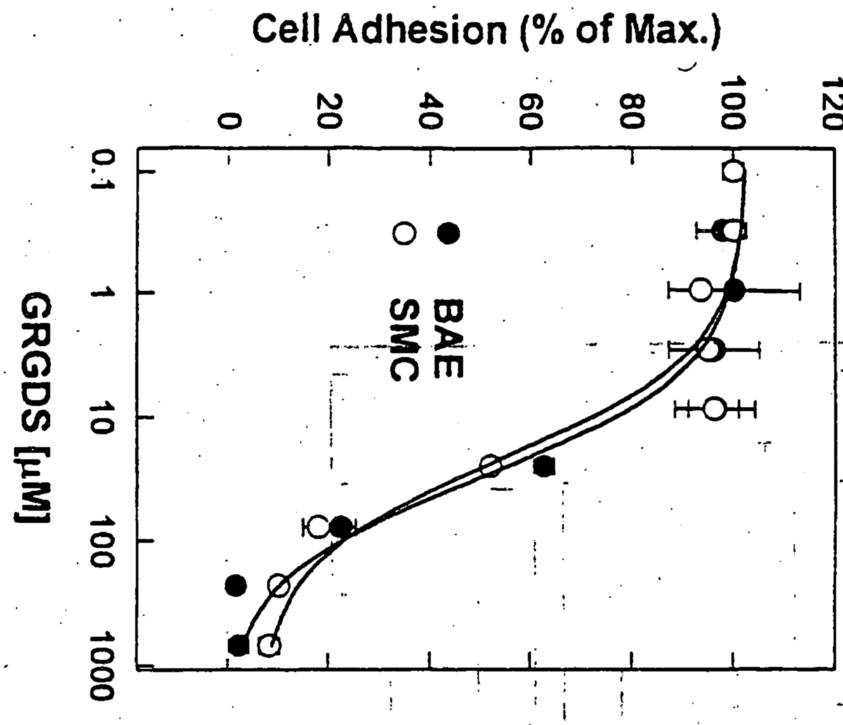


Fig. 49A

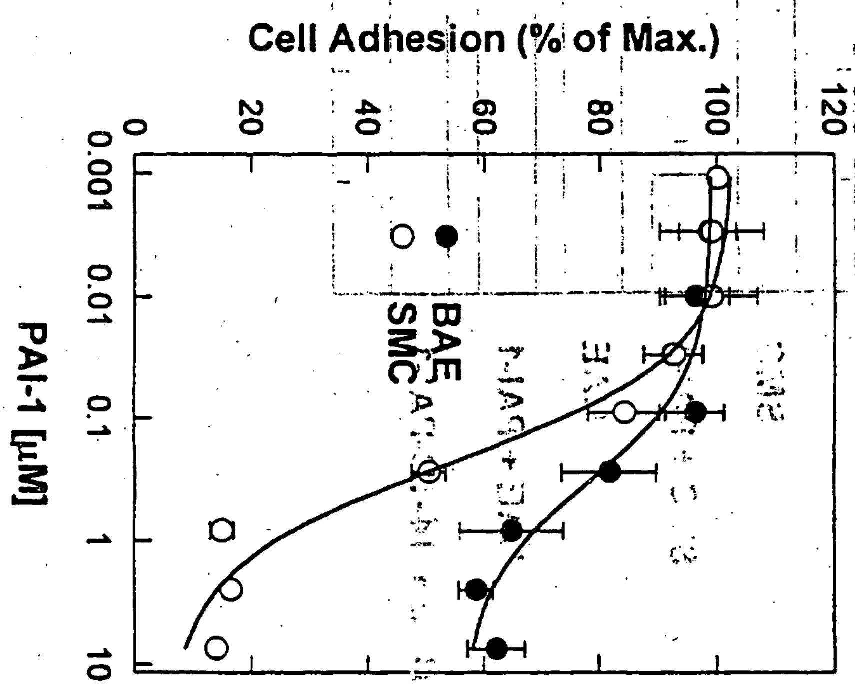


Fig. 49B

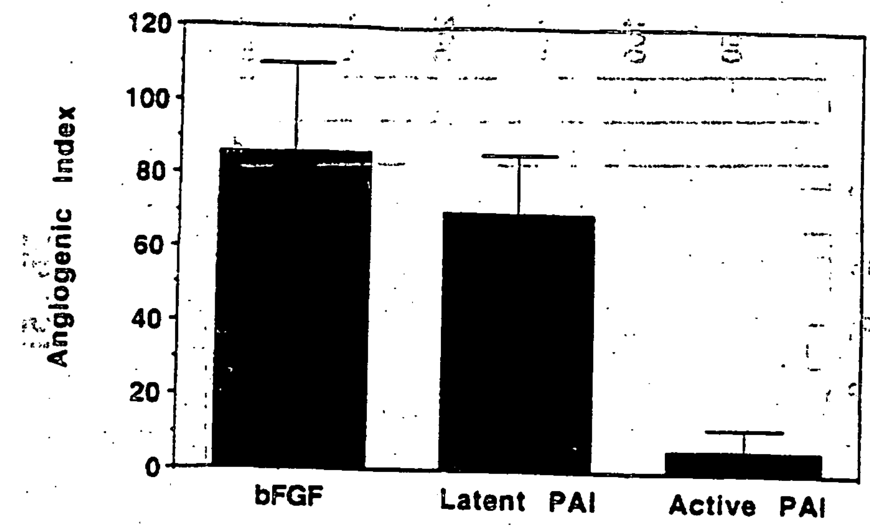


Fig. 50A

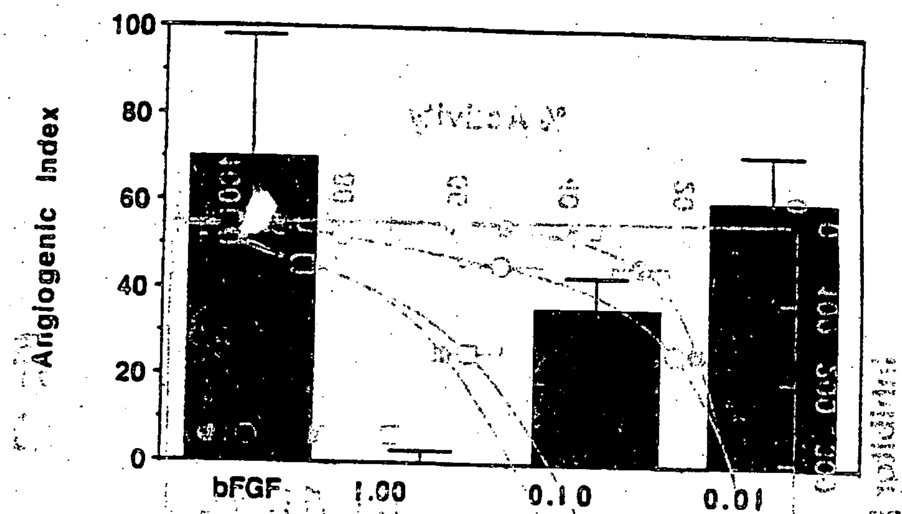


Fig. 50B

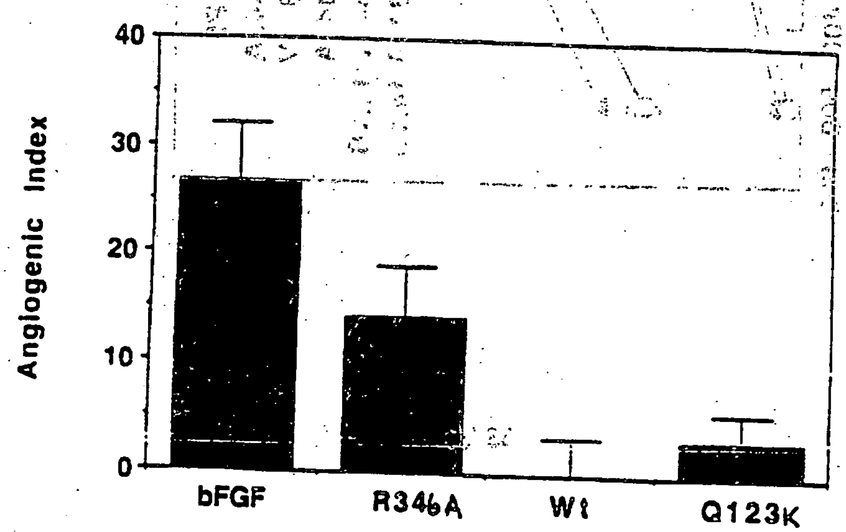


Fig. 50C

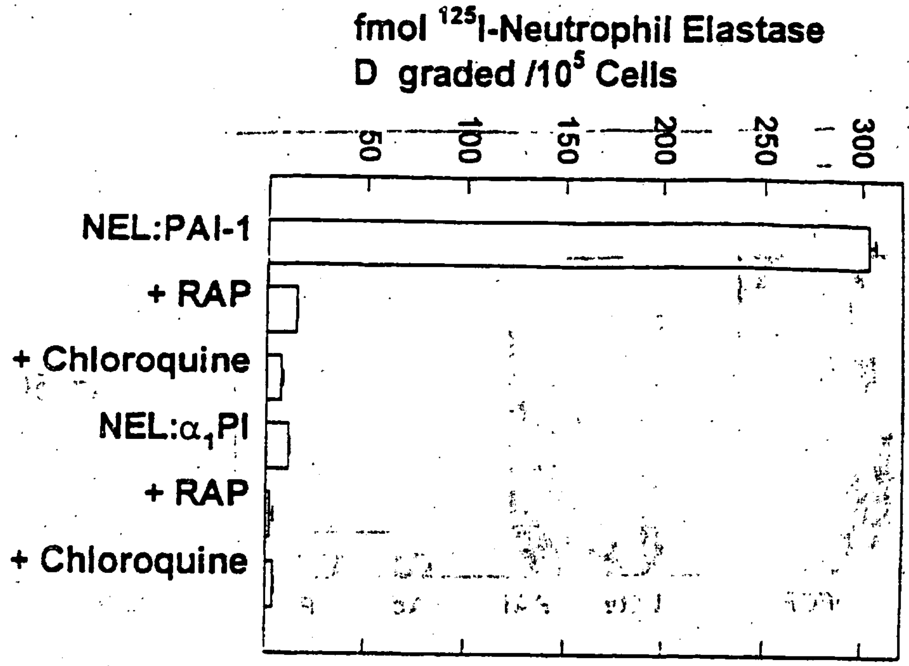

fmol ^{125}I-Neutrophil Elastase
D graded /10^5 Cells
50
100
150
200
250
300
NEL:PAI-1
+ RAP
+ Chloroquine
NEL:α$_1$PI
+ RAP
+ Chloroquine

Fig. 51

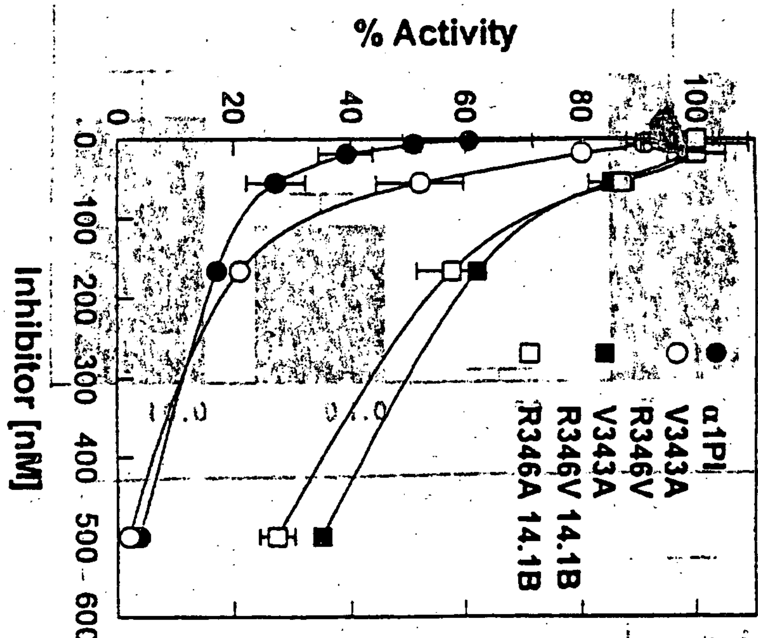

% Activity
0
20
40
60
80
100
0
100
200
300
400
500
600
Inhibitor [nM]
α1PI
V343A
R346V
V343A
R346V 14.1B
R346A 14.1B

Fig. 52

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06071

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07K 14/00, 16/00; C07H 04; A61K 38/00
US CL : 530/350, 387.1; 536/23.1; 514/2
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350, 387.1; 536/23.1; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOGUE
Search terms: plasminogen activator inhibitor type 1, PAI-1, mutant or variant, antibody

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	LAWRENCE et al. Engineering plasminogen activator inhibitor 1 mutants with increased functional stabillity. Biochemistry. 1994, Vol. 33, pages 3643-3648, see entire document.	1-32
X --- Y	BERKENPAS et al. Molecular evolution of plasminogen activator inhibitor-1 functional stability. The EMBO Journal. 1995, Vol. 14, No. 13, pages 2969-2977, see entire document.	9-13, 15, 18-20 --- 1-8, 14, 16-17, 21-32

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 JULY 1997	03 SEP 1997

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	MINH-TAM B. DAVIS
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y	CARRELL et al. The biostructural pathology of the serpins: Critical function of sheet opening mechanism. Biol. Chem. Hoppe-Seyler. January 1996, Vol. 377, pages 1-17, see entire document.	9-13, 15, 18-20 -- 1-8, 14, 16-17, 21-32
Y	REILLY et al. Recombinant plasminogen activator inhibitor type 1: a review of structural, functional, and biological aspects. Blood Coagulation and Fibrinolysis. 1994, Vol. 5, pages 73-81, See entire document.	3, 4
Y	LAWRENCE et al. Serpin reactive center loop mobility is required for inhibitor function but not for enzyme recognition. The Journal of Biological Chemistry. 04 November 1994, Vol.269, No. 44, pages 27657-27662, see entire document.	8
Y	SHORE et al. A fluorescent probe study of plasminogen activator inhibitor-1. The Journal of Biological Chemistry. 10 March 1995, Vol. 270, No. 10, pages 5395-5398. See entire document.	3-6
Y	VAN MEIJER et al. Determination of the vitronectin binding site on plasminogen activator inhibitor 1 (PAI-1). FEBS Letters. 1994, Vol. 352, pages 342-346, see entire document.	1-32
Y	SHUBEITA et al. Mutational and immunochemical analysis of plasminogen activator inhibitor 1. The Journal of Biological Chemistry. 25 October 1990, Vol. 265, No. 30, pages 18379-18385, see entire document.	31-32

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06071

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)1-30, drawn to a mutant PAI-1 protein, a pharmaceutical composition comprising said protein, its encoding DNA sequence, a host cell transformed with said DNA sequence, and a method for inhibiting elastase or cell attachment, or migration and/or migration-induced proliferation.
Group II, claim(s) 31-32, drawn to an antibody specific for an epitope of a mutant PAI-1 protein, which epitope is not present on wild-type PAI-1.

The inventions listed as Groups I-II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:
In the instant case, the shared inventive concept would appear to be a mutant PAI-1 protein. If the mutant PAI-1 protein is anticipated or obvious in view of the art, then there is no special technical feature linking the groups, and therefore no unity of invention. It appears that Lawrence, DA, et al, 1994, Biochemistry, 33: 3643-3648, and Berkenpas, MB et al, 1995, EMBO J., 14(13): 2969-2977 are obvious over group I. There is no neccessary technical feature linkage between a protein, and an antibody. Therefore, the invention of claims 1-32 do not fulfill the requirement for unity of invention, and each member form basis of an individual group.

(12) INTERNATIONAL APPLICATION PUBLISHED

(19) World Intellectual Property Organization
International Bureau

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(21) International Application Number: PCT/CA

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(71) Applicant: GENETICS INC. [CA/CA]; Toronto, Ontario

(72) Inventors; and
(75) Inventors/Applicants (for US only): TAWASHI, Toronto, Ontario (CA). PENAFIEL, (CA).

(74) Agents: KAI, Patrick; Sim & McBurney, 6th Floor, 330 University Avenue, Toronto, Ontario M5G 1R7 (CA).

(84) Designated States

Published:
— With international search report.

(88) Date of publication of the international search report:

(54) Title:

(57) Abstract: